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NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223966
Seq. ID	LIB3165-060-Q1-K1-F11
Method	BLASTX
NCBI GI	g3763916
BLAST score	331
E value	6.0e-31
Match length	126
% identity	53
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]
Seq. No.	223967
Seq. ID	LIB3165-060-Q1-K1-F12
Method	BLASTX
NCBI GI	g729668
BLAST score	242
E value	1.0e-20
Match length	55
% identity	84
NCBI Description	HISTONE H1 >gi_2147479_pir_S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.	223968
Seq. ID	LIB3165-060-Q1-K1-F3
Method	BLASTX
NCBI GI	g1352821
BLAST score	352
E value	1.0e-33
Match length	67
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.	223969
Seq. ID	LIB3165-060-Q1-K1-F5
Method	BLASTX
NCBI GI	g4455223
BLAST score	403
E value	2.0e-39
Match length	126
% identity	32
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]
Seq. No.	223970
Seq. ID	LIB3165-060-Q1-K1-F6

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Method BLASTX
 NCBI GI g464775
 BLAST score 447
 E value 1.0e-44
 Match length 89
 % identity 92
 NCBI Description SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir_S39492
 superoxide dismutase - Para rubber tree >gi_348137 (L11707)
 superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No. 223971
 Seq. ID LIB3165-060-Q1-K1-F7
 Method BLASTX
 NCBI GI g3549626
 BLAST score 294
 E value 1.0e-26
 Match length 99
 % identity 55
 NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No. 223972
 Seq. ID LIB3165-060-Q1-K1-G1
 Method BLASTX
 NCBI GI g289920
 BLAST score 429
 E value 1.0e-42
 Match length 82
 % identity 98
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 223973
 Seq. ID LIB3165-060-Q1-K1-G10
 Method BLASTX
 NCBI GI g1352821
 BLAST score 495
 E value 3.0e-50
 Match length 95
 % identity 98
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
 ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223974
 Seq. ID LIB3165-060-Q1-K1-G12
 Method BLASTX
 NCBI GI g1781348
 BLAST score 572
 E value 3.0e-59
 Match length 119
 % identity 92
 NCBI Description (Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No. 223975

Seq. ID LIB3165-060-Q1-K1-G2
Method BLASTX
NCBI GI g1170567
BLAST score 280
E value 3.0e-25
Match length 56
% identity 89
NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
>gi_1085960_pir_S52648 INO1 protein - Citrus paradisi
>gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No. 223976
Seq. ID LIB3165-060-Q1-K1-G4
Method BLASTX
NCBI GI g3687652
BLAST score 503
E value 3.0e-51
Match length 106
% identity 92
NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]

Seq. No. 223977
Seq. ID LIB3165-060-Q1-K1-G5
Method BLASTX
NCBI GI g1871192
BLAST score 140
E value 1.0e-08
Match length 64
% identity 44
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 223978
Seq. ID LIB3165-060-Q1-K1-G7
Method BLASTX
NCBI GI g1352821
BLAST score 302
E value 8.0e-28
Match length 63
% identity 94
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
(RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223979
Seq. ID LIB3165-060-Q1-K1-H1
Method BLASTX
NCBI GI g2980770
BLAST score 260
E value 5.0e-23
Match length 67
% identity 78
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 223980

053640185 201000

Seq. ID	LIB3165-060-Q1-K1-H11
Method	BLASTX
NCBI GI	g131393
BLAST score	350
E value	3.0e-33
Match length	106
% identity	72
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi_100360_pir_S15005 photosystem II oxygen-evolving complex protein 2 - common tobacco >gi_19911_emb_CAA39039.1_ (X55354) photosystem II 23kDa polypeptide [Nicotiana tabacum]
Seq. No.	223981
Seq. ID	LIB3165-060-Q1-K1-H12
Method	BLASTX
NCBI GI	g267122
BLAST score	422
E value	1.0e-41
Match length	100
% identity	77
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) >gi_478400_pir_JQ2242 thioredoxin h - Arabidopsis thaliana >gi_16552_emb_CAA78462_ (Z14084) Thioredoxin H [Arabidopsis thaliana] >gi_1388080_ (U35827) thioredoxin h [Arabidopsis thaliana]
Seq. No.	223982
Seq. ID	LIB3165-060-Q1-K1-H4
Method	BLASTX
NCBI GI	g120659
BLAST score	396
E value	1.0e-38
Match length	79
% identity	94
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST >gi_81721_pir_B24796 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13), chloroplast - white mustard (fragment) >gi_829288_emb_CAA27845_ (X04302) chloroplast GAPDH (233aa) [Sinapis alba]
Seq. No.	223983
Seq. ID	LIB3165-060-Q1-K1-H6
Method	BLASTX
NCBI GI	g1749546
BLAST score	222
E value	3.0e-18
Match length	77
% identity	60
NCBI Description	(D89169) similar to <i>Saccharomyces cerevisiae</i> SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]
Seq. No.	223984
Seq. ID	LIB3165-060-Q1-K1-H7

Method BLASTX
NCBI GI g1352821
BLAST score 320
E value 8.0e-30
Match length 63
% identity 97
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
(RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223985
Seq. ID LIB3165-060-Q1-K1-H9
Method BLASTX
NCBI GI g4406530
BLAST score 259
E value 5.0e-26
Match length 92
% identity 74
NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 223986
Seq. ID LIB3166-001-Q1-K1-A1
Method BLASTX
NCBI GI g4102600
BLAST score 543
E value 9.0e-56
Match length 124
% identity 86
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No. 223987
Seq. ID LIB3166-001-Q1-K1-A11
Method BLASTX
NCBI GI g2584721
BLAST score 631
E value 4.0e-66
Match length 139
% identity 83
NCBI Description (Y10157) sulfite reductase [Arabidopsis thaliana]

Seq. No. 223988
Seq. ID LIB3166-001-Q1-K1-A2
Method BLASTX
NCBI GI g967125
BLAST score 691
E value 4.0e-73
Match length 135
% identity 96
NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No. 223989
Seq. ID LIB3166-001-Q1-K1-A3
Method BLASTX
NCBI GI g1263291
BLAST score 556

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E value 2.0e-57
Match length 120
% identity 87
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 223990
Seq. ID LIB3166-001-Q1-K1-A5
Method BLASTX
NCBI GI g3169182
BLAST score 360
E value 2.0e-34
Match length 78
% identity 85
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 223991
Seq. ID LIB3166-001-Q1-K1-A6
Method BLASTX
NCBI GI g4455202
BLAST score 392
E value 5.0e-38
Match length 106
% identity 73
NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 223992
Seq. ID LIB3166-001-Q1-K1-A8
Method BLASTX
NCBI GI g2191129
BLAST score 301
E value 2.0e-27
Match length 135
% identity 55
NCBI Description (AF007269) similar to SPF1 DNA-binding protein [Arabidopsis thaliana]

Seq. No. 223993
Seq. ID LIB3166-001-Q1-K1-A9
Method BLASTX
NCBI GI g3046815
BLAST score 544
E value 7.0e-56
Match length 130
% identity 82
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 223994
Seq. ID LIB3166-001-Q1-K1-B1
Method BLASTX
NCBI GI g3122116
BLAST score 296
E value 8.0e-27
Match length 132
% identity 48
NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG
>gi_2660540_emb_CAA05102_ (AJ001932) cell cycle protein
[Helicobacter felis]

09/20/2000

Seq. No.	223995
Seq. ID	LIB3166-001-Q1-K1-B10
Method	BLASTX
NCBI GI	g3023195
BLAST score	605
E value	5.0e-63
Match length	135
% identity	88
NCBI Description	14-3-3-LIKE PROTEIN B (SGF14B) >gi_1575727 (U70534) SGF14B [Glycine max]
Seq. No.	223996
Seq. ID	LIB3166-001-Q1-K1-B11
Method	BLASTX
NCBI GI	g2541876
BLAST score	221
E value	5.0e-18
Match length	76
% identity	51
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
Seq. No.	223997
Seq. ID	LIB3166-001-Q1-K1-B3
Method	BLASTX
NCBI GI	g3608485
BLAST score	649
E value	3.0e-68
Match length	127
% identity	94
NCBI Description	(AF088915) proteasome beta subunit [Petunia x hybrida]
Seq. No.	223998
Seq. ID	LIB3166-001-Q1-K1-B7
Method	BLASTX
NCBI GI	g886116
BLAST score	516
E value	1.0e-52
Match length	131
% identity	70
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]
Seq. No.	223999
Seq. ID	LIB3166-001-Q1-K1-B9
Method	BLASTX
NCBI GI	g3955021
BLAST score	174
E value	2.0e-12
Match length	35
% identity	89
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]
Seq. No.	224000

Seq. No.	224001
Seq. ID	LIB3166-001-Q1-K1-C1
Method	BLASTX
NCBI GI	g3790567
BLAST score	196
E value	4.0e-15
Match length	116
% identity	36
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]
Seq. No.	224001
Seq. ID	LIB3166-001-Q1-K1-C11
Method	BLASTX
NCBI GI	g1495804
BLAST score	631
E value	4.0e-66
Match length	137
% identity	86
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.	224002
Seq. ID	LIB3166-001-Q1-K1-C12
Method	BLASTX
NCBI GI	g1170504
BLAST score	175
E value	1.0e-12
Match length	68
% identity	49
NCBI Description	EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82 (IEIF-(ISO)4F P82) >gi_452440 (M95747) initiation factor (iso)4f p82 subunit [Triticum aestivum]
Seq. No.	224003
Seq. ID	LIB3166-001-Q1-K1-C2
Method	BLASTX
NCBI GI	g4455340
BLAST score	235
E value	1.0e-19
Match length	65
% identity	68
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]
Seq. No.	224004
Seq. ID	LIB3166-001-Q1-K1-C3
Method	BLASTX
NCBI GI	g1408471
BLAST score	511
E value	5.0e-52
Match length	113
% identity	81
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]
Seq. No.	224005
Seq. ID	LIB3166-001-Q1-K1-C6
Method	BLASTX

NCBI GI g3021355
BLAST score 409
E value 5.0e-40
Match length 89
% identity 88
NCBI Description (AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No. 224006
Seq. ID LIB3166-001-Q1-K1-C7
Method BLASTX
NCBI GI g2829918
BLAST score 548
E value 2.0e-56
Match length 129
% identity 81
NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No. 224007
Seq. ID LIB3166-001-Q1-K1-C8
Method BLASTX
NCBI GI g4314378
BLAST score 343
E value 3.0e-32
Match length 136
% identity 51
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 224008
Seq. ID LIB3166-001-Q1-K1-D10
Method BLASTX
NCBI GI g4263712
BLAST score 408
E value 6.0e-40
Match length 98
% identity 77
NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 224009
Seq. ID LIB3166-001-Q1-K1-D11
Method BLASTX
NCBI GI g1706482
BLAST score 169
E value 6.0e-12
Match length 107
% identity 40
NCBI Description DNA LIGASE IV (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
>gi_860937_emb_CAA58467_(X83441) DNA ligase IV [Homo sapiens]
>gi_4504997_ref_NP_002303.1_pLIG4_ligase IV, DNA, ATP-dependent

Seq. No. 224010
Seq. ID LIB3166-001-Q1-K1-D3
Method BLASTX
NCBI GI g2459429

BLAST score 502
E value 6.0e-51
Match length 126
% identity 71
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 224011
Seq. ID LIB3166-001-Q1-K1-D5
Method BLASTX
NCBI GI g2501572
BLAST score 387
E value 2.0e-37
Match length 107
% identity 63
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545
(L47118) EMB8 gene product [Picea glauca]

Seq. No. 224012
Seq. ID LIB3166-001-Q1-K1-D6
Method BLASTX
NCBI GI g310587
BLAST score 160
E value 5.0e-11
Match length 51
% identity 65
NCBI Description (L20864) ascorbate peroxidase [Spinacia oleracea]
>gi_1384110_dbj_BAA12890_ (D85864) cytosolic ascorbate
peroxidase [Spinacia oleracea]

Seq. No. 224013
Seq. ID LIB3166-001-Q1-K1-D7
Method BLASTX
NCBI GI g4539348
BLAST score 142
E value 9.0e-09
Match length 50
% identity 80-
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No. 224014
Seq. ID LIB3166-001-Q1-K1-E1
Method BLASTX
NCBI GI g4249410
BLAST score 563
E value 4.0e-58
Match length 128
% identity 82
NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 224015
Seq. ID LIB3166-001-Q1-K1-E11
Method BLASTX
NCBI GI g2344901
BLAST score 252
E value 8.0e-22
Match length 84
% identity 64

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NCBI Description (AC002388) serine/threonine protein kinase isolog [Arabidopsis thaliana]

Seq. No. 224016
Seq. ID LIB3166-001-Q1-K1-E12
Method BLASTX
NCBI GI g3775989
BLAST score 557
E value 2.0e-57
Match length 137
% identity 75
NCBI Description (AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No. 224017
Seq. ID LIB3166-001-Q1-K1-E3
Method BLASTX
NCBI GI g4206789
BLAST score 457
E value 9.0e-46
Match length 129
% identity 71
NCBI Description (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No. 224018
Seq. ID LIB3166-001-Q1-K1-E7
Method BLASTX
NCBI GI g4204313
BLAST score 481
E value 2.0e-48
Match length 107
% identity 83
NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 224019
Seq. ID LIB3166-001-Q1-K1-E9
Method BLASTX
NCBI GI g136636
BLAST score 469
E value 4.0e-47
Match length 87
% identity 98
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
>gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No. 224020
Seq. ID LIB3166-001-Q1-K1-F10
Method BLASTX
NCBI GI g479406

BLAST score 404
E value 5.0e-50
Match length 119
% identity 62
NCBI Description chlorophyll a/b-binding protein - garden pea
>gi_20671_emb_CAA49149 (X69215) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No. 224021
Seq. ID LIB3166-001-Q1-K1-F11
Method BLASTX
NCBI GI g3281846
BLAST score 176
E value 1.0e-12
Match length 132
% identity 33
NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No. 224022
Seq. ID LIB3166-001-Q1-K1-F3
Method BLASTX
NCBI GI g3281848
BLAST score 188
E value 4.0e-14
Match length 132
% identity 46
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 224023
Seq. ID LIB3166-001-Q1-K1-F5
Method BLASTX
NCBI GI g2218152
BLAST score 693
E value 2.0e-73
Match length 136
% identity 90
NCBI Description (AF005279) type IIIa membrane protein cp-wap13 [Vigna unguiculata]

Seq. No. 224024
Seq. ID LIB3166-001-Q1-K1-G12
Method BLASTX
NCBI GI g3218467
BLAST score 221
E value 5.0e-18
Match length 138
% identity 38
NCBI Description (AJ006529) putative phosphatase [Gallus gallus]

Seq. No. 224025
Seq. ID LIB3166-001-Q1-K1-G2
Method BLASTX
NCBI GI g1854386
BLAST score 487
E value 3.0e-49
Match length 137
% identity 68

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No. 224026
Seq. ID LIB3166-001-Q1-K1-G3
Method BLASTX
NCBI GI g2780194
BLAST score 546
E value 4.0e-56
Match length 123
% identity 58

NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No. 224027
Seq. ID LIB3166-001-Q1-K1-G5
Method BLASTX
NCBI GI g4262250
BLAST score 370
E value 2.0e-35
Match length 108
% identity 74

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 224028
Seq. ID LIB3166-001-Q1-K1-G6
Method BLASTX
NCBI GI g3859116
BLAST score 360
E value 2.0e-34
Match length 120
% identity 59

NCBI Description (AF031609) unknown [Oryza sativa]

Seq. No. 224029
Seq. ID LIB3166-001-Q1-K1-G8
Method BLASTX
NCBI GI g1946369
BLAST score 142
E value 9.0e-09
Match length 84
% identity 44

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 224030
Seq. ID LIB3166-001-Q1-K1-G9
Method BLASTX
NCBI GI g1346769
BLAST score 501
E value 8.0e-51
Match length 136
% identity 65

NCBI Description PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
>gi_558596_emb_CAA52605 (X74496) prolyl oligopeptidase
[Homo sapiens] >gi_1585155_prf_2124300A Pro oligopeptidase
[Homo sapiens] >gi_4506043_ref_NP_002717.1_pPREP_ prolyl
endopeptidase

Seq. No. 224031
 Seq. ID LIB3166-001-Q1-K1-H2
 Method BLASTX
 NCBI GI g3402704
 BLAST score 344
 E value 2.0e-32
 Match length 119
 % identity 66
 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

 Seq. No. 224032
 Seq. ID LIB3166-001-Q1-K1-H4
 Method BLASTX
 NCBI GI g421836
 BLAST score 603
 E value 8.0e-63
 Match length 139
 % identity 84
 NCBI Description G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]

 Seq. No. 224033
 Seq. ID LIB3166-001-Q1-K1-H5
 Method BLASTX
 NCBI GI g2252631
 BLAST score 158
 E value 1.0e-10
 Match length 63
 % identity 49
 NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

 Seq. No. 224034
 Seq. ID LIB3166-001-Q1-K1-H6
 Method BLASTX
 NCBI GI g3319342
 BLAST score 164
 E value 2.0e-11
 Match length 45
 % identity 64
 NCBI Description (AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

 Seq. No. 224035
 Seq. ID LIB3166-001-Q1-K1-H7
 Method BLASTX
 NCBI GI g1352076
 BLAST score 162
 E value 4.0e-11
 Match length 134
 % identity 33
 NCBI Description BETA-GALACTOSIDASE (LACTASE) >gi_144746 (M35107) beta-D-galactosidase (cbgA) [Clostridium acetobutylicum]

 Seq. No. 224036
 Seq. ID LIB3166-001-Q1-K1-H8
 Method BLASTX

NCBI GI	g4262225
BLAST score	464
E value	2.0e-46
Match length	139
% identity	58
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]
Seq. No.	224037
Seq. ID	LIB3166-001-Q1-K2-A1
Method	BLASTX
NCBI GI	g4102600
BLAST score	543
E value	8.0e-56
Match length	124
% identity	86
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.	224038
Seq. ID	LIB3166-001-Q1-K3-A1
Method	BLASTX
NCBI GI	g4102600
BLAST score	543
E value	8.0e-56
Match length	124
% identity	86
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.	224039
Seq. ID	LIB3166-001-Q1-K3-A2
Method	BLASTX
NCBI GI	g1220196
BLAST score	535
E value	7.0e-55
Match length	115
% identity	88
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.	224040
Seq. ID	LIB3166-001-Q1-K3-A3
Method	BLASTX
NCBI GI	g3122116
BLAST score	266
E value	2.0e-23
Match length	123
% identity	48
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG >gi_2660540_emb_CAA05102_ (AJ001932) cell cycle protein [Helicobacter felis]
Seq. No.	224041
Seq. ID	LIB3166-001-Q1-K3-A7
Method	BLASTX
NCBI GI	g3169182
BLAST score	360
E value	2.0e-34
Match length	78

```

% identity 85
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 224042
Seq. ID LIB3166-001-Q1-K3-B1
Method BLASTX
NCBI GI g3608485
BLAST score 597
E value 4.0e-62
Match length 117
% identity 95
NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No. 224043
Seq. ID LIB3166-001-Q1-K3-B11
Method BLASTX
NCBI GI g3859116
BLAST score 223
E value 6.0e-29
Match length 121
% identity 64
NCBI Description (AF031609) unknown [Oryza sativa]

Seq. No. 224044
Seq. ID LIB3166-001-Q1-K3-B2
Method BLASTX
NCBI GI g3790567
BLAST score 161
E value 5.0e-11
Match length 108
% identity 33
NCBI Description (AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No. 224045
Seq. ID LIB3166-001-Q1-K3-B3
Method BLASTX
NCBI GI g1408471
BLAST score 455
E value 1.0e-45
Match length 102
% identity 79
NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No. 224046
Seq. ID LIB3166-001-Q1-K3-B5
Method BLASTX
NCBI GI g1854386
BLAST score 462
E value 2.0e-46
Match length 127
% identity 69
NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

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Seq. No.	224047
Seq. ID	LIB3166-001-Q1-K3-B7
Method	BLASTX
NCBI GI	g886116
BLAST score	481
E value	1.0e-48
Match length	124
% identity	69
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]
Seq. No.	224048
Seq. ID	LIB3166-001-Q1-K3-B9
Method	BLASTX
NCBI GI	g2829918
BLAST score	511
E value	4.0e-52
Match length	121
% identity	80
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]
Seq. No.	224049
Seq. ID	LIB3166-001-Q1-K3-C1
Method	BLASTX
NCBI GI	g1545805
BLAST score	159
E value	5.0e-11
Match length	89
% identity	48
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]
Seq. No.	224050
Seq. ID	LIB3166-001-Q1-K3-C11
Method	BLASTX
NCBI GI	g4262225
BLAST score	304
E value	6.0e-28
Match length	108
% identity	51
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]
Seq. No.	224051
Seq. ID	LIB3166-001-Q1-K3-C2
Method	BLASTX
NCBI GI	g2459429
BLAST score	461
E value	3.0e-46
Match length	116
% identity	73
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]
Seq. No.	224052
Seq. ID	LIB3166-001-Q1-K3-C3
Method	BLASTX

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NCBI GI g4249410
 BLAST score 519
 E value 5.0e-53
 Match length 119
 % identity 81
 NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 224053
 Seq. ID LIB3166-001-Q1-K3-C4
 Method BLASTX
 NCBI GI g3402704
 BLAST score 312
 E value 1.0e-28
 Match length 107
 % identity 67
 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224054
 Seq. ID LIB3166-001-Q1-K3-C7
 Method BLASTX
 NCBI GI g2501572
 BLAST score 387
 E value 2.0e-37
 Match length 107
 % identity 63
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545
 (L47118) EMB8 gene product [Picea glauca]

Seq. No. 224055
 Seq. ID LIB3166-001-Q1-K3-D1
 Method BLASTX
 NCBI GI g4206789
 BLAST score 517
 E value 7.0e-53
 Match length 123
 % identity 82
 NCBI Description (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No. 224056
 Seq. ID LIB3166-001-Q1-K3-D3
 Method BLASTX
 NCBI GI g3281848
 BLAST score 164
 E value 2.0e-11
 Match length 113
 % identity 46
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 224057
 Seq. ID LIB3166-001-Q1-K3-D7
 Method BLASTX
 NCBI GI g4204313
 BLAST score 414
 E value 9.0e-41
 Match length 91
 % identity 85

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NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 224058
Seq. ID LIB3166-001-Q1-K3-D8
Method BLASTX
NCBI GI g2218152
BLAST score 531
E value 2.0e-54
Match length 125
% identity 78

NCBI Description (AF005279) type IIIa membrane protein cp-wap13 [Vigna unguiculata]

Seq. No. 224059
Seq. ID LIB3166-001-Q1-K3-E2
Method BLASTX
NCBI GI g2780194
BLAST score 336
E value 1.0e-41
Match length 107
% identity 86

NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No. 224060
Seq. ID LIB3166-001-Q1-K3-E7
Method BLASTX
NCBI GI g4262250
BLAST score 312
E value 9.0e-29
Match length 96
% identity 72

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 224061
Seq. ID LIB3166-001-Q1-K3-F2
Method BLASTX
NCBI GI g1399273
BLAST score 619
E value 9.0e-65
Match length 123
% identity 94

NCBI Description (U31834) calmodulin-domain protein kinase CDPK isoform 5 [Arabidopsis thaliana] >gi_3080419_emb_CAA18738_ (AL022604) calmodulin-domain protein kinase CDPK isoform 5 (CPK5) [Arabidopsis thaliana]

Seq. No. 224062
Seq. ID LIB3166-001-Q1-K3-F7
Method BLASTX
NCBI GI g98554
BLAST score 150
E value 9.0e-10
Match length 119
% identity 34

NCBI Description beta-galactosidase (EC 3.2.1.23) - Clostridium acetobutylicum

096640461000

Seq. No. 224063
Seq. ID LIB3166-001-Q1-K3-F8
Method BLASTX
NCBI GI g4455202
BLAST score 327
E value 2.0e-30
Match length 109
% identity 60
NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 224064
Seq. ID LIB3166-001-Q1-K3-F9
Method BLASTX
NCBI GI g2191129
BLAST score 225
E value 1.0e-18
Match length 115
% identity 51
NCBI Description (AF007269) similar to SPF1 DNA-binding protein [Arabidopsis thaliana]

Seq. No. 224065
Seq. ID LIB3166-001-Q1-K3-G3
Method BLASTX
NCBI GI g4455340
BLAST score 172
E value 2.0e-12
Match length 64
% identity 58
NCBI Description (AL035522) putative protein [Arabidopsis thaliana]

Seq. No. 224066
Seq. ID LIB3166-001-Q1-K3-G9
Method BLASTX
NCBI GI g3021355
BLAST score 409
E value 4.0e-40
Match length 89
% identity 88
NCBI Description (AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No. 224067
Seq. ID LIB3166-001-Q1-K3-H7
Method BLASTX
NCBI GI g4314378
BLAST score 293
E value 2.0e-26
Match length 124
% identity 48
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 224068
Seq. ID LIB3166-001-Q1-K3-H8
Method BLASTX
NCBI GI g310587

BLAST score 143
E value 6.0e-09
Match length 51
% identity 59
NCBI Description (L20864) ascorbate peroxidase [Spinacia oleracea]
>gi_1384110 dbj_BAA12890_ (D85864) cytosolic ascorbate peroxidase [Spinacia oleracea]

Seq. No. 224069
Seq. ID LIB3166-002-Q1-K1-A10
Method BLASTX
NCBI GI g4539301
BLAST score 247
E value 3.0e-21
Match length 68
% identity 74
NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 224070
Seq. ID LIB3166-002-Q1-K1-A2
Method BLASTX
NCBI GI g2827524
BLAST score 366
E value 3.0e-35
Match length 77
% identity 82
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 224071
Seq. ID LIB3166-002-Q1-K1-A3
Method BLASTX
NCBI GI g3249081
BLAST score 347
E value 9.0e-33
Match length 136
% identity 11
NCBI Description (AC004473) Strong similarity to AR0GP2 gene gb_1762634 from Lycopersicon esculentum. [Arabidopsis thaliana]

Seq. No. 224072
Seq. ID LIB3166-002-Q1-K1-A4
Method BLASTX
NCBI GI g4510430
BLAST score 498
E value 2.0e-50
Match length 107
% identity 85
NCBI Description (AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No. 224073
Seq. ID LIB3166-002-Q1-K1-A6
Method BLASTX
NCBI GI g2558938
BLAST score 234
E value 9.0e-20

Match length 93
% identity 55
NCBI Description (AF024625) arm repeat containing protein [Brassica napus]

Seq. No. 224074
Seq. ID LIB3166-002-Q1-K1-A7
Method BLASTX
NCBI GI g4105782
BLAST score 293
E value 2.0e-26
Match length 67
% identity 87
NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]

Seq. No. 224075
Seq. ID LIB3166-002-Q1-K1-A8
Method BLASTX
NCBI GI g3461846
BLAST score 372
E value 1.0e-35
Match length 108
% identity 30
NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No. 224076
Seq. ID LIB3166-002-Q1-K1-A9
Method BLASTX
NCBI GI g1762428
BLAST score 356
E value 8.0e-34
Match length 94
% identity 68
NCBI Description (U59467) aromatic rich glycoprotein JP630 [Arabidopsis thaliana]

Seq. No. 224077
Seq. ID LIB3166-002-Q1-K1-B1
Method BLASTX
NCBI GI g3688123
BLAST score 395
E value 2.0e-38
Match length 120
% identity 66
NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No. 224078
Seq. ID LIB3166-002-Q1-K1-B10
Method BLASTX
NCBI GI g418507
BLAST score 167
E value 1.0e-11
Match length 71
% identity 48
NCBI Description S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir_S40872 hypothetical

protein f161 - Escherichia coli >gi_305032 (L19201)
ORF_f161 [Escherichia coli] >gi_1336002 (U56082)
S-adenosylmethionine:2-demethylmenaquinone
methyltransferase [Escherichia coli] >gi_1790364 (AE000467)
menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No. 224079
Seq. ID LIB3166-002-Q1-K1-B2
Method BLASTX
NCBI GI g3688123
BLAST score 352
E value 2.0e-33
Match length 122
% identity 61
NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No. 224080
Seq. ID LIB3166-002-Q1-K1-B3
Method BLASTX
NCBI GI g3559811
BLAST score 498
E value 2.0e-50
Match length 137
% identity 72
NCBI Description (AJ010735) grl-protein [Arabidopsis thaliana]

Seq. No. 224081
Seq. ID LIB3166-002-Q1-K1-B4
Method BLASTX
NCBI GI g1483563
BLAST score 157
E value 1.0e-10
Match length 39
% identity 74
NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No. 224082
Seq. ID LIB3166-002-Q1-K1-B5
Method BLASTX
NCBI GI g1666096
BLAST score 453
E value 3.0e-45
Match length 129
% identity 73
NCBI Description (Y09113) dioxygenase [Marah macrocarpus]

Seq. No. 224083
Seq. ID LIB3166-002-Q1-K1-B8
Method BLASTX
NCBI GI g2827528
BLAST score 460
E value 5.0e-46
Match length 117
% identity 74
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	224084
Seq. ID	LIB3166-002-Q1-K1-B9
Method	BLASTX
NCBI GI	g1170031
BLAST score	634
E value	2.0e-66
Match length	135
% identity	89
NCBI Description	GLUTAMATE-1-SEMALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_541940_pir_JQ2263 glutamate 1-semialdehyde aminotransferase (EC 2.6.1.-) precursor - soybean >gi_310567 (L12453) glutamate 1-semialdehyde aminotransferase [Glycine max] >gi_747968 (U20260) glutamate 1-semialdehyde aminotransferase [Glycine max]
Seq. No.	224085
Seq. ID	LIB3166-002-Q1-K1-C1
Method	BLASTX
NCBI GI	g1707018
BLAST score	456
E value	1.0e-45
Match length	132
% identity	70
NCBI Description	(U78721) CutA isolog [Arabidopsis thaliana]
Seq. No.	224086
Seq. ID	LIB3166-002-Q1-K1-C10
Method	BLASTX
NCBI GI	g3859536
BLAST score	626
E value	2.0e-65
Match length	125
% identity	90
NCBI Description	(AF095453) asparagine synthetase [Arabidopsis thaliana]
Seq. No.	224087
Seq. ID	LIB3166-002-Q1-K1-C11
Method	BLASTX
NCBI GI	g4469020
BLAST score	469
E value	4.0e-47
Match length	123
% identity	76
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]
Seq. No.	224088
Seq. ID	LIB3166-002-Q1-K1-C12
Method	BLASTX
NCBI GI	g1255954
BLAST score	534
E value	1.0e-54
Match length	118
% identity	83
NCBI Description	(Z70677) thioredoxin [Ricinus communis]

Seq. No. 224089
Seq. ID LIB3166-002-Q1-K1-C2
Method BLASTX
NCBI GI g3603401
BLAST score 288
E value 7.0e-26
Match length 126
% identity 49
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No. 224090
Seq. ID LIB3166-002-Q1-K1-C3
Method BLASTX
NCBI GI g2829870
BLAST score 275
E value 2.0e-24
Match length 117
% identity 58
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 224091
Seq. ID LIB3166-002-Q1-K1-C4
Method BLASTX
NCBI GI g1708934
BLAST score 176
E value 9.0e-13
Match length 60
% identity 50
NCBI Description CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) >gi_2137198_pir_A57235 CDK-activating kinase p36 - mouse >gi_1015999 (U35249) CDK-activating kinase assembly factor p36/MAT1 [Mus musculus]

Seq. No. 224092
Seq. ID LIB3166-002-Q1-K1-C7
Method BLASTX
NCBI GI g1709007
BLAST score 187
E value 5.0e-14
Match length 107
% identity 40
NCBI Description O-SUCCINYLHOMOSERINE SULFHYDRYLASE (OSH SULFHYDRYLASE) >gi_607830 (U10904) O-succinylhomoserine sulfhydrylase [Pseudomonas aeruginosa]

Seq. No. 224093
Seq. ID LIB3166-002-Q1-K1-D10
Method BLASTX
NCBI GI g3242789
BLAST score 549
E value 2.0e-56
Match length 114
% identity 87
NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No.	224094
Seq. ID	LIB3166-002-Q1-K1-D11
Method	BLASTX
NCBI GI	g1469930
BLAST score	294
E value	1.0e-26
Match length	92
% identity	70
NCBI Description	(U48777) fiber-specific acyl carrier protein [Gossypium hirsutum]
Seq. No.	224095
Seq. ID	LIB3166-002-Q1-K1-D2
Method	BLASTX
NCBI GI	g4432859
BLAST score	326
E value	2.0e-30
Match length	106
% identity	61
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]
Seq. No.	224096
Seq. ID	LIB3166-002-Q1-K1-D4
Method	BLASTX
NCBI GI	g3024126
BLAST score	524
E value	1.0e-53
Match length	102
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_1655576_emb_CAA95856_(Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]
Seq. No.	224097
Seq. ID	LIB3166-002-Q1-K1-D5
Method	BLASTX
NCBI GI	g3877579
BLAST score	216
E value	2.0e-17
Match length	108
% identity	49
NCBI Description	(Z82271) Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes fr... >gi_3879321_emb_CAB07273_(Z92811) Similarity to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes fr
Seq. No.	224098
Seq. ID	LIB3166-002-Q1-K1-D6
Method	BLASTX
NCBI GI	g4455159
BLAST score	181

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E value 1.0e-20
Match length 72
% identity 62
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 224099
Seq. ID LIB3166-002-Q1-K1-D7
Method BLASTX
NCBI GI g4416347
BLAST score 416
E value 7.0e-41
Match length 87
% identity 92
NCBI Description (AF109403) MADS C-2 protein; MADS-box protein [Sinapis alba]

Seq. No. 224100
Seq. ID LIB3166-002-Q1-K1-D9
Method BLASTX
NCBI GI g4559358
BLAST score 208
E value 2.0e-16
Match length 65
% identity 57
NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No. 224101
Seq. ID LIB3166-002-Q1-K1-E1
Method BLASTX
NCBI GI g516118
BLAST score 221
E value 5.0e-18
Match length 125
% identity 43
NCBI Description (L08469) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 224102
Seq. ID LIB3166-002-Q1-K1-E10
Method BLASTX
NCBI GI g2827143
BLAST score 621
E value 6.0e-65
Match length 137
% identity 84
NCBI Description (AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 224103
Seq. ID LIB3166-002-Q1-K1-E11
Method BLASTX
NCBI GI g3046815
BLAST score 468
E value 6.0e-47
Match length 93
% identity 90
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 224104
 Seq. ID LIB3166-002-Q1-K1-E12
 Method BLASTX
 NCBI GI g3953465
 BLAST score 116
 E value 8.0e-12
 Match length 91
 % identity 51
 NCBI Description (AC002328) F20N2.10 [Arabidopsis thaliana]

 Seq. No. 224105
 Seq. ID LIB3166-002-Q1-K1-E4
 Method BLASTX
 NCBI GI g3434971
 BLAST score 240
 E value 3.0e-20
 Match length 62
 % identity 71
 NCBI Description (AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]

 Seq. No. 224106
 Seq. ID LIB3166-002-Q1-K1-E5
 Method BLASTX
 NCBI GI g2982303
 BLAST score 205
 E value 4.0e-16
 Match length 46
 % identity 87
 NCBI Description (AF051236) hypothetical protein [Picea mariana]

 Seq. No. 224107
 Seq. ID LIB3166-002-Q1-K1-E6
 Method BLASTX
 NCBI GI g4432857
 BLAST score 190
 E value 2.0e-14
 Match length 106
 % identity 46
 NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

 Seq. No. 224108
 Seq. ID LIB3166-002-Q1-K1-E8
 Method BLASTX
 NCBI GI g4049348
 BLAST score 271
 E value 2.0e-26
 Match length 136
 % identity 46
 NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

 Seq. No. 224109
 Seq. ID LIB3166-002-Q1-K1-E9
 Method BLASTX
 NCBI GI g3983665
 BLAST score 516

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E value 1.0e-52
Match length 129
% identity 80
NCBI Description (AB011271) importin-beta2 [Oryza sativa]

Seq. No. 224110
Seq. ID LIB3166-002-Q1-K1-F10
Method BLASTX
NCBI GI g3834310
BLAST score 520
E value 1.0e-53
Match length 115
% identity 96
NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122
come from this gene. [Arabidopsis thaliana]

Seq. No. 224111
Seq. ID LIB3166-002-Q1-K1-F12
Method BLASTX
NCBI GI g3928084
BLAST score 377
E value 3.0e-36
Match length 136
% identity 57
NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No. 224112
Seq. ID LIB3166-002-Q1-K1-F3
Method BLASTX
NCBI GI g2970641
BLAST score 664
E value 6.0e-70
Match length 129
% identity 94
NCBI Description (AF052194) xyloglucan endotransglycosylase precursor
[Actinidia deliciosa]

Seq. No. 224113
Seq. ID LIB3166-002-Q1-K1-F4
Method BLASTX
NCBI GI g3434973
BLAST score 219
E value 8.0e-18
Match length 76
% identity 61
NCBI Description (AB008106) ethylene responsive element binding factor 4
[Arabidopsis thaliana]

Seq. No. 224114
Seq. ID LIB3166-002-Q1-K1-F5
Method BLASTX
NCBI GI g1076515
BLAST score 258
E value 2.0e-22

095647010000

Match length 115
% identity 49
NCBI Description pectinesterase precursor - kidney bean
>gi_732913_emb_CAA59482_ (X85216) pectinesterase [Phaseolus vulgaris]

Seq. No. 224115
Seq. ID LIB3166-002-Q1-K1-F8
Method BLASTX
NCBI GI g2642448
BLAST score 384
E value 3.0e-37
Match length 118
% identity 29
NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]
>gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224116
Seq. ID LIB3166-002-Q1-K1-G10
Method BLASTX
NCBI GI g710626
BLAST score 287
E value 9.0e-26
Match length 86
% identity 65
NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No. 224117
Seq. ID LIB3166-002-Q1-K1-G11
Method BLASTX
NCBI GI g710626
BLAST score 187
E value 3.0e-14
Match length 79
% identity 53
NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No. 224118
Seq. ID LIB3166-002-Q1-K1-G3
Method BLASTX
NCBI GI g4572679
BLAST score 388
E value 1.0e-37
Match length 106
% identity 69
NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 224119
Seq. ID LIB3166-002-Q1-K1-G4

Method BLASTX
NCBI GI g3962377
BLAST score 523
E value 2.0e-53
Match length 121
% identity 85
NCBI Description (AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No. 224120
Seq. ID LIB3166-002-Q1-K1-G7
Method BLASTX
NCBI GI g4572679
BLAST score 234
E value 8.0e-20
Match length 67
% identity 66
NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 224121
Seq. ID LIB3166-002-Q1-K1-H12
Method BLASTX
NCBI GI g1332579
BLAST score 393
E value 2.0e-56
Match length 121
% identity 10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 224122
Seq. ID LIB3166-002-Q1-K1-H3
Method BLASTX
NCBI GI g266946
BLAST score 233
E value 9.0e-20
Match length 54
% identity 85
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN) >gi_71143_pir_R5UBP0 acidic ribosomal protein P0 - red goosefoot >gi_18141_emb_CAA33276_ (X15206) 34kD light-induced protein [Chenopodium rubrum]

Seq. No. 224123
Seq. ID LIB3166-002-Q1-K1-H4
Method BLASTX
NCBI GI g100351
BLAST score 437
E value 2.0e-43
Match length 130
% identity 65
NCBI Description pathogenesis-related protein 4A - common tobacco >gi_19962_emb_CAA41437_ (X58546) pathogenesis-related protein 4A [Nicotiana tabacum]

Seq. No. 224124
Seq. ID LIB3166-002-Q1-K1-H6
Method BLASTX

NCBI GI g3955021
BLAST score 423
E value 1.0e-41
Match length 96
% identity 85
NCBI Description (AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No. 224125
Seq. ID LIB3166-002-Q1-K1-H7
Method BLASTX
NCBI GI g2738949
BLAST score 335
E value 1.0e-31
Match length 68
% identity 90
NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No. 224126
Seq. ID LIB3166-002-Q1-K1-H8
Method BLASTX
NCBI GI g70644
BLAST score 562
E value 5.0e-58
Match length 124
% identity 18
NCBI Description ubiquitin precursor - common sunflower (fragment)

Seq. No. 224127
Seq. ID LIB3166-003-P1-K1-A10
Method BLASTX
NCBI GI g3757521
BLAST score 492
E value 9.0e-50
Match length 143
% identity 64
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 224128
Seq. ID LIB3166-003-P1-K1-A2
Method BLASTX
NCBI GI g4539370
BLAST score 221
E value 3.0e-18
Match length 59
% identity 71
NCBI Description (AL049525) UDP-galactose 4-epimerase-like protein [Arabidopsis thaliana]

Seq. No. 224129
Seq. ID LIB3166-003-P1-K1-A3
Method BLASTX
NCBI GI g224293
BLAST score 386
E value 2.0e-37
Match length 78

% identity	100
NCBI Description	histone H4 [Triticum aestivum]
Seq. No.	224130
Seq. ID	LIB3166-003-P1-K1-B1
Method	BLASTX
NCBI GI	g3335060
BLAST score	150
E value	1.0e-09
Match length	110
% identity	36
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
Seq. No.	224131
Seq. ID	LIB3166-003-P1-K1-B12
Method	BLASTX
NCBI GI	g2146797
BLAST score	429
E value	2.0e-42
Match length	138
% identity	40
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi_1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi_1587210_prf_2206331A protein disulfide isomerase [Ricinus communis]
Seq. No.	224132
Seq. ID	LIB3166-003-P1-K1-B2
Method	BLASTX
NCBI GI	g2244999
BLAST score	220
E value	7.0e-18
Match length	96
% identity	47
NCBI Description	(Z97341) similarity to phaseolin G-box binding protein PG2 [Arabidopsis thaliana]
Seq. No.	224133
Seq. ID	LIB3166-003-P1-K1-B8
Method	BLASTX
NCBI GI	g131399
BLAST score	442
E value	5.0e-44
Match length	105
% identity	79
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir_S00411 photosystem II 10K protein precursor - potato >gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum tuberosum]
Seq. No.	224134
Seq. ID	LIB3166-003-P1-K1-C1
Method	BLASTX
NCBI GI	g3176726

BLAST score 299
E value 4.0e-27
Match length 82
% identity 76
NCBI Description (AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No. 224135
Seq. ID LIB3166-003-P1-K1-C12
Method BLASTX
NCBI GI g1174162
BLAST score 638
E value 7.0e-67
Match length 121
% identity 93
NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2
ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No. 224136
Seq. ID LIB3166-003-P1-K1-C2
Method BLASTX
NCBI GI g4218011
BLAST score 518
E value 8.0e-53
Match length 130
% identity 75
NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]
>gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 224137
Seq. ID LIB3166-003-P1-K1-C4
Method BLASTX
NCBI GI g3600031
BLAST score 226
E value 1.0e-18
Match length 111
% identity 51
NCBI Description (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana]

Seq. No. 224138
Seq. ID LIB3166-003-P1-K1-C9
Method BLASTX
NCBI GI g2244734
BLAST score 710
E value 2.0e-75
Match length 142
% identity 99
NCBI Description (D88414) actin [Gossypium hirsutum]

Seq. No. 224139
Seq. ID LIB3166-003-P1-K1-D10
Method BLASTX
NCBI GI g3122049
BLAST score 206

E value 1.0e-17
Match length 123
% identity 46
NCBI Description DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
>gi_1330236_dbj_BAA11189_ (D78011) dihydropyrimidinase
[Homo sapiens] >gi_3608122_dbj_BAA33067_ (AB004678)
dihydropyrimidinase [Homo sapiens]
>gi_4503375 ref NP_001376.1_pDPYS dihydropyrimidinase

Seq. No. 224140
Seq. ID LIB3166-003-P1-K1-D11
Method BLASTX
NCBI GI g4455208
BLAST score 554
E value 5.0e-57
Match length 138
% identity 78
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 224141
Seq. ID LIB3166-003-P1-K1-D4
Method BLASTX
NCBI GI g466172
BLAST score 146
E value 3.0e-09
Match length 61
% identity 52
NCBI Description GTP-BINDING PROTEIN YPTM2 >gi_283056_pir_B38202 ypt family - maize >gi_287835_emb CAA44919 (X63278) yptm2 [Zea mays]

Seq. No. 224142
Seq. ID LIB3166-003-P1-K1-D8
Method BLASTX
NCBI GI g3935168
BLAST score 223
E value 2.0e-25
Match length 122
% identity 54
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 224143
Seq. ID LIB3166-003-P1-K1-E6
Method BLASTX
NCBI GI g3688191
BLAST score 201
E value 1.0e-15
Match length 84
% identity 52
NCBI Description (AJ010090) MAP3K alpha protein kinase [Arabidopsis thaliana]

Seq. No. 224144
Seq. ID LIB3166-003-P1-K1-E7
Method BLASTX
NCBI GI g4115377
BLAST score 428
E value 2.0e-42

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Match length 100
 % identity 79
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

 Seq. No. 224145
 Seq. ID LIB3166-003-P1-K1-F2
 Method BLASTX
 NCBI GI g115833
 BLAST score 308
 E value 6.0e-44
 Match length 130
 % identity 66
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

 Seq. No. 224146
 Seq. ID LIB3166-003-P1-K1-F5
 Method BLASTX
 NCBI GI g3142290
 BLAST score 487
 E value 3.0e-49
 Match length 126
 % identity 80
 NCBI Description (AC002411) Contains similarity to gb_Z69902 from C. elegans. [Arabidopsis thaliana]

 Seq. No. 224147
 Seq. ID LIB3166-003-P1-K1-F6
 Method BLASTX
 NCBI GI g2244865
 BLAST score 158
 E value 1.0e-10
 Match length 127
 % identity 33
 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

 Seq. No. 224148
 Seq. ID LIB3166-003-P1-K1-G10
 Method BLASTX
 NCBI GI g3860263
 BLAST score 330
 E value 9.0e-31
 Match length 126
 % identity 56
 NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

 Seq. No. 224149
 Seq. ID LIB3166-003-P1-K1-G2
 Method BLASTX
 NCBI GI g3201541
 BLAST score 245
 E value 2.0e-21
 Match length 50
 % identity 90

NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]

Seq. No. 224150
Seq. ID LIB3166-003-P1-K1-G5
Method BLASTX
NCBI GI g2894534
BLAST score 243
E value 2.0e-34
Match length 100
% identity 79

NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 224151
Seq. ID LIB3166-003-P1-K1-G6
Method BLASTX
NCBI GI g2245066
BLAST score 180
E value 9.0e-14
Match length 55
% identity 60

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 224152
Seq. ID LIB3166-003-P1-K1-G7
Method BLASTX
NCBI GI g1730630
BLAST score 207
E value 2.0e-16
Match length 134
% identity 37

NCBI Description HYPOTHETICAL 82.6 KD PROTEIN B0361.8 IN CHROMOSOME III
>gi_458956 (U00031) similar to cytoplasmic domain of
synaptobrevin [Caenorhabditis elegans]

Seq. No. 224153
Seq. ID LIB3166-003-P1-K1-H10
Method BLASTX
NCBI GI g1142621
BLAST score 219
E value 9.0e-18
Match length 139
% identity 44

NCBI Description (U18349) phaseolin G-box binding protein PG2 [Phaseolus vulgaris]

Seq. No. 224154
Seq. ID LIB3166-003-P1-K1-H12
Method BLASTX
NCBI GI g1657948
BLAST score 180
E value 1.0e-13
Match length 37
% identity 86

NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 224155
Seq. ID LIB3166-003-P1-K1-H2

0956340116104000

Method BLASTX
NCBI GI g1351135
BLAST score 280
E value 2.0e-29
Match length 90
% identity 75
NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
>gi_436792_emb_CAA50317_ (X70990) sucrose synthase
[Arabidopsis thaliana]

Seq. No. 224156
Seq. ID LIB3166-003-P1-K1-H6
Method BLASTX
NCBI GI g1657948
BLAST score 137
E value 9.0e-09
Match length 41
% identity 66
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 224157
Seq. ID LIB3166-003-P1-K1-H9
Method BLASTX
NCBI GI g1174592
BLAST score 734
E value 4.0e-78
Match length 142
% identity 99
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
- garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
sativum]

Seq. No. 224158
Seq. ID LIB3166-004-P1-K1-A12
Method BLASTX
NCBI GI g586339
BLAST score 158
E value 1.0e-10
Match length 58
% identity 47
NCBI Description PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir_S46098
probable AMP-binding protein - yeast (Saccharomyces
cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c
[Saccharomyces cerevisiae]

Seq. No. 224159
Seq. ID LIB3166-004-P1-K1-A4
Method BLASTX
NCBI GI g2244916
BLAST score 160
E value 7.0e-11
Match length 131
% identity 31
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224160
Seq. ID LIB3166-004-P1-K1-A6

Method BLASTX
 NCBI GI g2190548
 BLAST score 229
 E value 3.0e-21
 Match length 81
 % identity 65
 NCBI Description (AC001229) EST gb_ATTS1121 comes from this gene.
 [Arabidopsis thaliana]

Seq. No. 224161
 Seq. ID LIB3166-004-P1-K1-A7
 Method BLASTX
 NCBI GI g3551999
 BLAST score 364
 E value 7.0e-35.
 Match length 102
 % identity 58
 NCBI Description (AF085081) alcohol dehydrogenase A [Gossypium hirsutum]
 >gi_3552001 (AF085082) alcohol dehydrogenase A [Gossypium hirsutum]
 >gi_4140628 (AF090163) alcohol dehydrogenase A [Gossypium hirsutum]
 >gi_4140630 (AF090164) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No. 224162
 Seq. ID LIB3166-004-P1-K1-A9
 Method BLASTX
 NCBI GI g3914442
 BLAST score 359
 E value 3.0e-34
 Match length 99
 % identity 73
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
 >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No. 224163
 Seq. ID LIB3166-004-P1-K1-B1
 Method BLASTX
 NCBI GI g1351014
 BLAST score 339
 E value 8.0e-32
 Match length 72
 % identity 89
 NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)
 ribosomal protein S8 [Oryza sativa]

Seq. No. 224164
 Seq. ID LIB3166-004-P1-K1-B11
 Method BLASTX
 NCBI GI g3759184
 BLAST score 272
 E value 5.0e-24
 Match length 121
 % identity 50
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 224165

Seq. ID LIB3166-004-P1-K1-B12
Method BLASTX
NCBI GI g1279542
BLAST score 505
E value 2.0e-51
Match length 118
% identity 89
NCBI Description (Z71276) small GTPase [Mangifera indica]

Seq. No. 224166
Seq. ID LIB3166-004-P1-K1-B3
Method BLASTX
NCBI GI g4538939
BLAST score 300
E value 4.0e-52
Match length 125
% identity 89
NCBI Description (AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No. 224167
Seq. ID LIB3166-004-P1-K1-B8
Method BLASTX
NCBI GI g3402683
BLAST score 146
E value 3.0e-09
Match length 39
% identity 74
NCBI Description (AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No. 224168
Seq. ID LIB3166-004-P1-K1-C1
Method BLASTX
NCBI GI g2130024
BLAST score 350
E value 4.0e-33
Match length 103
% identity 62
NCBI Description DNA-binding protein ABF2 - wild oat
>gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No. 224169
Seq. ID LIB3166-004-P1-K1-C10
Method BLASTX
NCBI GI g2129604
BLAST score 210
E value 1.0e-16
Match length 58
% identity 74
NCBI Description GTP-binding protein 1 - Arabidopsis thaliana
>gi_2129607_pir_S71584 GTP-binding protein ATBG1 -
Arabidopsis thaliana >gi_1184981 (U46924) ATGB1
[Arabidopsis thaliana]

Seq. No. 224170
Seq. ID LIB3166-004-P1-K1-C11

Method	BLASTX
NCBI GI	g3850583
BLAST score	330
E value	8.0e-31
Match length	125
% identity	56
NCBI Description	(AC005278) Contains similarity to transcription initiation factor IIE, alpha subunit gb_X63468 from Homo sapiens. [Arabidopsis thaliana]
Seq. No.	224171
Seq. ID	LIB3166-004-P1-K1-C12
Method	BLASTX
NCBI GI	g1931640
BLAST score	454
E value	3.0e-45
Match length	124
% identity	66
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]
Seq. No.	224172
Seq. ID	LIB3166-004-P1-K1-C5
Method	BLASTX
NCBI GI	g2102696
BLAST score	228
E value	8.0e-19
Match length	110
% identity	40
NCBI Description	(U72761) karyopherin beta 3 [Homo sapiens] >gi_4504909_ref_NP_002262.1_pKPNB3_ karyopherin (importin) beta
Seq. No.	224173
Seq. ID	LIB3166-004-P1-K1-C6
Method	BLASTX
NCBI GI	g3687243
BLAST score	249
E value	3.0e-21
Match length	68
% identity	72
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]
Seq. No.	224174
Seq. ID	LIB3166-004-P1-K1-D5
Method	BLASTX
NCBI GI	g1173218
BLAST score	575
E value	2.0e-59
Match length	113
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.	224175

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Seq. ID LIB3166-004-P1-K1-D6
 Method BLASTX
 NCBI GI g232024
 BLAST score 301
 E value 2.0e-27
 Match length 85
 % identity 69
 NCBI Description PROTEIN E6 >gi_421806_pir_A46130 fiber protein - upland cotton >gi_2129498_pir_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No. 224176
 Seq. ID LIB3166-004-P1-K1-D7
 Method BLASTX
 NCBI GI g3068705
 BLAST score 201
 E value 7.0e-16
 Match length 64
 % identity 69
 NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 224177
 Seq. ID LIB3166-004-P1-K1-E1
 Method BLASTX
 NCBI GI g1171579
 BLAST score 273
 E value 1.0e-24
 Match length 66
 % identity 80
 NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 224178
 Seq. ID LIB3166-004-P1-K1-E10
 Method BLASTX
 NCBI GI g4185740
 BLAST score 354
 E value 1.0e-33
 Match length 139
 % identity 56
 NCBI Description (AF079999) putative glutamate receptor [Arabidopsis thaliana]

Seq. No. 224179
 Seq. ID LIB3166-004-P1-K1-F12
 Method BLASTX
 NCBI GI g541881
 BLAST score 306
 E value 4.0e-28
 Match length 75
 % identity 73
 NCBI Description MYB homolog transcription ATMYB2 - Arabidopsis thaliana >gi_506189_dbj_BAA03534 (D14712) ATMYB2 [Arabidopsis thaliana] >gi_2275197 (AC002337) Atmyb2 [Arabidopsis thaliana]

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Seq. No.	224180
Seq. ID	LIB3166-004-P1-K1-F5
Method	BLASTX
NCBI GI	g4510375
BLAST score	460
E value	5.0e-46
Match length	116
% identity	77
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]
Seq. No.	224181
Seq. ID	LIB3166-004-P1-K1-F8
Method	BLASTX
NCBI GI	g2443891
BLAST score	163
E value	3.0e-11
Match length	116
% identity	49
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]
Seq. No.	224182
Seq. ID	LIB3166-004-P1-K1-G10
Method	BLASTX
NCBI GI	g2347199
BLAST score	176
E value	9.0e-13
Match length	72
% identity	64
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]
Seq. No.	224183
Seq. ID	LIB3166-004-P1-K1-G11
Method	BLASTX
NCBI GI	g4538911
BLAST score	379
E value	1.0e-36
Match length	120
% identity	63
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224184
Seq. ID	LIB3166-004-P1-K1-G3
Method	BLASTX
NCBI GI	g2970051
BLAST score	225
E value	1.0e-18
Match length	63
% identity	63
NCBI Description	(AB012110) ARG10 [Vigna radiata]
Seq. No.	224185
Seq. ID	LIB3166-004-P1-K1-G4
Method	BLASTX
NCBI GI	g1531758
BLAST score	174
E value	2.0e-12

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Match length 36
% identity 78
NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
unknown protein [Arabidopsis thaliana]

Seq. No. 224186
Seq. ID LIB3166-004-P1-K1-G6
Method BLASTX
NCBI GI g1174592
BLAST score 629
E value 7.0e-66
Match length 118
% identity 97
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
- garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
sativum]

Seq. No. 224187
Seq. ID LIB3166-004-P1-K1-G7
Method BLASTX
NCBI GI g3004555
BLAST score 316
E value 4.0e-29
Match length 136
% identity 5
NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis
thaliana]

Seq. No. 224188
Seq. ID LIB3166-004-P1-K1-H2
Method BLASTX
NCBI GI g1653702
BLAST score 254
E value 5.0e-22
Match length 80
% identity 65
NCBI Description (D90915) dihydrolipoamide acetyltransferase component (E2)
of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No. 224189
Seq. ID LIB3166-004-P1-K1-H5
Method BLASTX
NCBI GI g3582342
BLAST score 278
E value 1.0e-24
Match length 139
% identity 44
NCBI Description (AC005496) putative flavonol 3-o-glucosyltransferase
[Arabidopsis thaliana]

Seq. No. 224190
Seq. ID LIB3166-005-P1-K1-A1
Method BLASTX
NCBI GI g3046696
BLAST score 289
E value 2.0e-37
Match length 113

09624036-20400000

% identity	73
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]
Seq. No.	224191
Seq. ID	LIB3166-005-P1-K1-A11
Method	BLASTX
NCBI GI	g4056494
BLAST score	438
E value	2.0e-43
Match length	108
% identity	76
NCBI Description	(AC005896) putative protein translocase [Arabidopsis thaliana]
Seq. No.	224192
Seq. ID	LIB3166-005-P1-K1-A12
Method	BLASTX
NCBI GI	g2262178
BLAST score	277
E value	1.0e-24
Match length	129
% identity	50
NCBI Description	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]
Seq. No.	224193
Seq. ID	LIB3166-005-P1-K1-A2
Method	BLASTX
NCBI GI	g2642648
BLAST score	715
E value	6.0e-76
Match length	143
% identity	98
NCBI Description	(AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]
Seq. No.	224194
Seq. ID	LIB3166-005-P1-K1-A3
Method	BLASTX
NCBI GI	g2661021
BLAST score	594
E value	9.0e-62
Match length	117
% identity	95
NCBI Description	(AF035255) catalase [Glycine max]
Seq. No.	224195
Seq. ID	LIB3166-005-P1-K1-A4
Method	BLASTX
NCBI GI	g1297190
BLAST score	413
E value	2.0e-40
Match length	103
% identity	77
NCBI Description	(U53501) Theoretical protein with similarity to GenBank Accession Number L22302 serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 224196
Seq. ID LIB3166-005-P1-K1-A8
Method BLASTX
NCBI GI g1345684
BLAST score 455
E value 2.0e-45
Match length 105
% identity 85
NCBI Description CATALASE ISOZYME 3 >gi_536787_emb_CAA85426_ (Z36977)
catalase [Nicotiana plumbaginifolia]

Seq. No. 224197
Seq. ID LIB3166-005-P1-K1-A9
Method BLASTX
NCBI GI g2078350
BLAST score 255
E value 6.0e-22
Match length 119
% identity 51
NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 224198
Seq. ID LIB3166-005-P1-K1-B1
Method BLASTX
NCBI GI g3776559
BLAST score 323
E value 6.0e-30
Match length 109
% identity 54
NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933
cdc2 protein kinase homolog from A. thaliana BAC
gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
gene. [Arabidopsis thaliana]

Seq. No. 224199
Seq. ID LIB3166-005-P1-K1-B11
Method BLASTX
NCBI GI g729092
BLAST score 662
E value 1.0e-69
Match length 134
% identity 92
NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK)
>gi_477484_pir_A49082 calcium-dependent protein kinase
isoform AK1 - Arabidopsis thaliana >gi_304105 (L14771)
calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No. 224200
Seq. ID LIB3166-005-P1-K1-B12
Method BLASTX
NCBI GI g1168446
BLAST score 495
E value 4.0e-50
Match length 123
% identity 76

NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi_1073840_pir_F64132 aminopeptidase N (pepN) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20) >gi_1574460 (U32835) aminopeptidase N (pepN) [Haemophilus influenzae Rd]
Seq. No.	224201
Seq. ID	LIB3166-005-P1-K1-B3
Method	BLASTX
NCBI GI	g1326161
BLAST score	142
E value	1.0e-08
Match length	55
% identity	60
NCBI Description	(U54703) dehydrin [Phaseolus vulgaris]
Seq. No.	224202
Seq. ID	LIB3166-005-P1-K1-B7
Method	BLASTX
NCBI GI	g548770
BLAST score	165
E value	1.0e-11
Match length	63
% identity	60
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [<i>Oryza sativa</i>]
Seq. No.	224203
Seq. ID	LIB3166-005-P1-K1-C11
Method	BLASTX
NCBI GI	g100200
BLAST score	160
E value	4.0e-11
Match length	72
% identity	51
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.	224204
Seq. ID	LIB3166-005-P1-K1-C2
Method	BLASTX
NCBI GI	g4539348
BLAST score	359
E value	4.0e-34
Match length	123
% identity	54
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.	224205
Seq. ID	LIB3166-005-P1-K1-C3
Method	BLASTX
NCBI GI	g418854
BLAST score	622
E value	5.0e-65
Match length	131
% identity	17
NCBI Description	ubiquitin precursor - parsley >gi_288112_emb_CAA45621

(X64344) polyubiquitin [Petroselinum crispum]
>gi_288114_emb_CAA45622_ (X64345) polyubiquitin
[Petroselinum crispum]

Seq. No. 224206
Seq. ID LIB3166-005-P1-K1-D1
Method BLASTX
NCBI GI g225242
BLAST score 154
E value 2.0e-10
Match length 36
% identity 86
NCBI Description ORF 1708 [Nicotiana tabacum]

Seq. No. 224207
Seq. ID LIB3166-005-P1-K1-D11
Method BLASTX
NCBI GI g1946220
BLAST score 180
E value 3.0e-13
Match length 34
% identity 94
NCBI Description (Z71979) kn1-like protein [Malus domestica]

Seq. No. 224208
Seq. ID LIB3166-005-P1-K1-D12
Method BLASTX
NCBI GI g3901012
BLAST score 199
E value 1.0e-15
Match length 44
% identity 75
NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 224209
Seq. ID LIB3166-005-P1-K1-D5
Method BLASTX
NCBI GI g3249084
BLAST score 236
E value 2.0e-34
Match length 155
% identity 29
NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene
gb_X92750 from Mus musculus. ESTs gb_AA712687 and
gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No. 224210
Seq. ID LIB3166-005-P1-K1-D6
Method BLASTX
NCBI GI g4559372
BLAST score 357
E value 6.0e-34
Match length 87
% identity 76
NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana]

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Seq. No.	224211
Seq. ID	LIB3166-005-P1-K1-E1
Method	BLASTX
NCBI GI	g1076708
BLAST score	619
E value	1.0e-64
Match length	126
% identity	28
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf_2111434A tetraubiquitin [Helianthus annuus]
Seq. No.	224212
Seq. ID	LIB3166-005-P1-K1-E12
Method	BLASTX
NCBI GI	g3928095
BLAST score	399
E value	8.0e-54
Match length	138
% identity	76
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]
Seq. No.	224213
Seq. ID	LIB3166-005-P1-K1-E3
Method	BLASTX
NCBI GI	g951427
BLAST score	453
E value	3.0e-45
Match length	134
% identity	61
NCBI Description	(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]
Seq. No.	224214
Seq. ID	LIB3166-005-P1-K1-E4
Method	BLASTX
NCBI GI	g951427
BLAST score	539
E value	3.0e-55
Match length	135
% identity	75
NCBI Description	(M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]
Seq. No.	224215
Seq. ID	LIB3166-005-P1-K1-E5
Method	BLASTX
NCBI GI	g134945
BLAST score	444
E value	4.0e-44
Match length	134

% identity	64
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) (DELTA(9) STEAROYL-ACYL CARRIER PROTEIN DESATURASE) >gi_66360_pir_OHCSAD acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) precursor - castor bean >gi_21093_emb_CAA39859_ (X56508) acyl-[acyl-carrier protein] desatu [Ricinus communis] >gi_228313_prf_1802405A stearoyl acyl carrier desaturase [Ricinus communis]
Seq. No.	224216
Seq. ID	LIB3166-005-P1-K1-E6
Method	BLASTX
NCBI GI	g1703129
BLAST score	578
E value	7.0e-60
Match length	114
% identity	95
NCBI Description	ACTIN 11 >gi_2129522_pir_S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]
Seq. No.	224217
Seq. ID	LIB3166-005-P1-K1-E9
Method	BLASTX
NCBI GI	g4455318
BLAST score	327
E value	9.0e-31
Match length	88
% identity	72
NCBI Description	(AL035528) glycine hydroxymethyltransferase-like protein [Arabidopsis thaliana]
Seq. No.	224218
Seq. ID	LIB3166-005-P1-K1-F1
Method	BLASTX
NCBI GI	g3559816
BLAST score	699
E value	5.0e-74
Match length	142
% identity	93
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]
Seq. No.	224219
Seq. ID	LIB3166-005-P1-K1-F10
Method	BLASTX
NCBI GI	g4105794
BLAST score	298
E value	5.0e-27
Match length	79
% identity	62
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]
Seq. No.	224220
Seq. ID	LIB3166-005-P1-K1-F11
Method	BLASTX
NCBI GI	g4468978

BLAST score 356
E value 8.0e-34
Match length 139
% identity 55
NCBI Description (AL035605) peroxidase-like protein [Arabidopsis thaliana]

Seq. No. 224221
Seq. ID LIB3166-005-P1-K1-F3
Method BLASTX
NCBI GI g4063749
BLAST score 116
E value 4.0e-11
Match length 91
% identity 46
NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224222
Seq. ID LIB3166-005-P1-K1-F5
Method BLASTX
NCBI GI g4455276
BLAST score 502
E value 6.0e-51
Match length 143
% identity 72
NCBI Description (AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No. 224223
Seq. ID LIB3166-005-P1-K1-F6
Method BLASTX
NCBI GI g1076715
BLAST score 196
E value 4.0e-15
Match length 86
% identity 41
NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No. 224224
Seq. ID LIB3166-005-P1-K1-G7
Method BLASTX
NCBI GI g1769903
BLAST score 347
E value 9.0e-33
Match length 140
% identity 54
NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No. 224225
Seq. ID LIB3166-005-P1-K1-G8
Method BLASTX
NCBI GI g1220196
BLAST score 311
E value 6.0e-56
Match length 129
% identity 85
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

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Seq. No. 224226
Seq. ID LIB3166-005-P1-K1-H10
Method BLASTX
NCBI GI g1694976
BLAST score 337
E value 1.0e-31
Match length 74
% identity 84
NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]
>gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No. 224227
Seq. ID LIB3166-005-P1-K1-H12
Method BLASTX
NCBI GI g3688123
BLAST score 436
E value 3.0e-43
Match length 119
% identity 71
NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No. 224228
Seq. ID LIB3166-005-P1-K1-H3
Method BLASTX
NCBI GI g3036951
BLAST score 390
E value 5.0e-38
Match length 74
% identity 100
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 224229
Seq. ID LIB3166-005-P1-K1-H4
Method BLASTX
NCBI GI g3193327
BLAST score 223
E value 3.0e-18
Match length 84
% identity 56
NCBI Description (AF069299) No definition line found [Arabidopsis thaliana]

Seq. No. 224230
Seq. ID LIB3166-005-P1-K1-H5
Method BLASTX
NCBI GI g2494842
BLAST score 148
E value 3.0e-10
Match length 79
% identity 48
NCBI Description GLUCOSYLTRANSFERASE ALG6 >gi_2131171_pir_S61985 ALG6
protein - yeast (Saccharomyces cerevisiae) >gi_1150997
(U43491) hypothetical protein UNA544 [Saccharomyces cerevisiae] >gi_1420090_emb_CAA99190_ (Z74910) ORF YOR002w

[Saccharomyces cerevisiae]

09624016-201000

Seq. No.	224231
Seq. ID	LIB3166-005-P1-K1-H6
Method	BLASTX
NCBI GI	g170354
BLAST score	538
E value	3.0e-55
Match length	109
% identity	21
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.	224232
Seq. ID	LIB3166-005-P1-K1-H7
Method	BLASTX
NCBI GI	g3928529
BLAST score	152
E value	9.0e-16
Match length	88
% identity	53
NCBI Description	(AB015502) alcohol dehydrogenase [Arabis hirsuta]
Seq. No.	224233
Seq. ID	LIB3166-005-P1-K1-H8
Method	BLASTX
NCBI GI	g2493146
BLAST score	223
E value	3.0e-18
Match length	61
% identity	75
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_755148 (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275) vacuolar H+-ATPase c subunit [Citrus unshiu]
Seq. No.	224234
Seq. ID	LIB3166-005-P1-K1-H9
Method	BLASTX
NCBI GI	g2244732
BLAST score	751
E value	4.0e-80
Match length	141
% identity	99
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.	224235
Seq. ID	LIB3166-006-P1-K1-A10
Method	BLASTX
NCBI GI	g2827709
BLAST score	280
E value	6.0e-25
Match length	133
% identity	47
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	224236
Seq. ID	LIB3166-006-P1-K1-A11

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Method	BLASTX
NCBI GI	g3319921
BLAST score	190
E value	1.0e-14
Match length	60
% identity	63
NCBI Description	(AJ223388) Hev b 3 [Hevea brasiliensis] >gi_3319923_emb_CAA11304 (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305 (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber particle protein [Hevea brasiliensis]
Seq. No.	224237
Seq. ID	LIB3166-006-P1-K1-A12
Method	BLASTX
NCBI GI	g3335366
BLAST score	190
E value	1.0e-14
Match length	80
% identity	46
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.	224238
Seq. ID	LIB3166-006-P1-K1-A2
Method	BLASTX
NCBI GI	g3122785
BLAST score	410
E value	2.0e-40
Match length	88
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]
Seq. No.	224239
Seq. ID	LIB3166-006-P1-K1-A3
Method	BLASTX
NCBI GI	g4249385
BLAST score	263
E value	1.0e-44
Match length	99
% identity	90
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]
Seq. No.	224240
Seq. ID	LIB3166-006-P1-K1-A4
Method	BLASTX
NCBI GI	g117988
BLAST score	521
E value	3.0e-53
Match length	99
% identity	95
NCBI Description	CYTOCHROME C >gi_65503_pir_CCCN cytochrome c - sea-island cotton
Seq. No.	224241
Seq. ID	LIB3166-006-P1-K1-A7
Method	BLASTX

056602631000

NCBI GI	g4490321
BLAST score	169
E value	4.0e-12
Match length	70
% identity	51
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]
Seq. No.	224242
Seq. ID	LIB3166-006-P1-K1-A9
Method	BLASTX
NCBI GI	g2392769
BLAST score	145
E value	3.0e-12
Match length	87
% identity	52
NCBI Description	(AC002534) putative histone deacetylase [Arabidopsis thaliana]
Seq. No.	224243
Seq. ID	LIB3166-006-P1-K1-B1
Method	BLASTX
NCBI GI	g4512698
BLAST score	548
E value	2.0e-56
Match length	112
% identity	91
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224244
Seq. ID	LIB3166-006-P1-K1-B10
Method	BLASTX
NCBI GI	g1076365
BLAST score	218
E value	4.0e-18
Match length	76
% identity	57
NCBI Description	pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis thaliana >gi_2129666_pir_JC4778 pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana >gi_550306_emb_CAA57275_(X81585) ATPME1 [Arabidopsis thaliana] >gi_903895_(U25649) ATPME1 precursor [Arabidopsis thaliana]
Seq. No.	224245
Seq. ID	LIB3166-006-P1-K1-B11
Method	BLASTX
NCBI GI	g3790100
BLAST score	422
E value	8.0e-42
Match length	94
% identity	90
NCBI Description	(AF095520) pyrophosphate-dependent phosphofructokinase beta subunit [Citrus X paradisi]
Seq. No.	224246
Seq. ID	LIB3166-006-P1-K1-B12
Method	BLASTX
NCBI GI	g2244900

BLAST score 366
E value 2.0e-41
Match length 132
% identity 61
NCBI Description (297338) similarity to hypothetical protein HYP1
Arabidopsis [Arabidopsis thaliana]

Seq. No. 224247
Seq. ID LIB3166-006-P1-K1-B2
Method BLASTX
NCBI GI g125887
BLAST score 157
E value 1.0e-10
Match length 89
% identity 37
NCBI Description ANOTHER SPECIFIC LAT52 PROTEIN PRECURSOR
>gi_82092_pir_S04765 LAT52 protein precursor - tomato
>gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]

Seq. No. 224248
Seq. ID LIB3166-006-P1-K1-B4
Method BLASTX
NCBI GI g1332579
BLAST score 486
E value 2.0e-52
Match length 115
% identity 10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 224249
Seq. ID LIB3166-006-P1-K1-B5
Method BLASTX
NCBI GI g4218122
BLAST score 276
E value 1.0e-24
Match length 95
% identity 61
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 224250
Seq. ID LIB3166-006-P1-K1-C1
Method BLASTX
NCBI GI g2213643
BLAST score 250
E value 1.0e-28
Match length 91
% identity 71
NCBI Description (U57338) glossy1 homolog [Oryza sativa]

Seq. No. 224251
Seq. ID LIB3166-006-P1-K1-C11
Method BLASTX
NCBI GI g2065531
BLAST score 254
E value 5.0e-22
Match length 81

% identity 64
 NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 224252
 Seq. ID LIB3166-006-P1-K1-C12
 Method BLASTX
 NCBI GI g1345787
 BLAST score 678
 E value 1.0e-71
 Match length 134
 % identity 94
 NCBI Description CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)
 >gi_567937_dbj_BAA05641_ (D26594) chalcone synthase
 [Camellia sinensis]

Seq. No. 224253
 Seq. ID LIB3166-006-P1-K1-C4
 Method BLASTX
 NCBI GI g2244732
 BLAST score 446
 E value 2.0e-44
 Match length 90
 % identity 94
 NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No. 224254
 Seq. ID LIB3166-006-P1-K1-C5
 Method BLASTX
 NCBI GI g2979551
 BLAST score 174
 E value 9.0e-13
 Match length 57
 % identity 65
 NCBI Description (AC003680) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 224255
 Seq. ID LIB3166-006-P1-K1-C7
 Method BLASTX
 NCBI GI g128190
 BLAST score 530
 E value 2.0e-54
 Match length 122
 % identity 80
 NCBI Description NITRATE REDUCTASE 2 (NR2) >gi_66205_pir_RDNTNS nitrate
 reductase (NADH) (EC 1.6.6.1) nia-2 - common tobacco
 >gi_19891_emb_CAA32217_ (X14059) nitrate reductase
 [Nicotiana tabacum]

Seq. No. 224256
 Seq. ID LIB3166-006-P1-K1-D1
 Method BLASTX
 NCBI GI g4490341
 BLAST score 172
 E value 3.0e-12
 Match length 124
 % identity 39

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NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 224257
Seq. ID LIB3166-006-P1-K1-D10
Method BLASTX
NCBI GI g3249084
BLAST score 185
E value 3.0e-14
Match length 58
% identity 29

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene
gb_X92750 from Mus musculus. ESTs gb_AA712687 and
gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No. 224258
Seq. ID LIB3166-006-P1-K1-D11
Method BLASTX
NCBI GI g3738285
BLAST score 278
E value 9.0e-25
Match length 69
% identity 75

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 224259
Seq. ID LIB3166-006-P1-K1-D12
Method BLASTX
NCBI GI g1173256
BLAST score 629
E value 7.0e-66
Match length 123
% identity 98

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal
protein S4 - upland cotton >gi_488739_emb_CAA55882
(X79300) ribosomal protein, small subunit 4e (RS4e)
[Gossypium hirsutum]

Seq. No. 224260
Seq. ID LIB3166-006-P1-K1-D6
Method BLASTX
NCBI GI g2078350
BLAST score 173
E value 7.0e-15
Match length 54
% identity 81

NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 224261
Seq. ID LIB3166-006-P1-K1-D7
Method BLASTX
NCBI GI g1749596
BLAST score 252
E value 2.0e-27
Match length 101
% identity 61

NCBI Description (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT
Accession Number P16638 [Schizosaccharomyces pombe]

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Seq. No. 224262
Seq. ID LIB3166-006-P1-K1-D9
Method BLASTX
NCBI GI g2505870
BLAST score 575
E value 1.0e-59
Match length 128
% identity 89
NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224263
Seq. ID LIB3166-006-P1-K1-E10
Method BLASTX
NCBI GI g4468993
BLAST score 302
E value 2.0e-27
Match length 134
% identity 51
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 224264
Seq. ID LIB3166-006-P1-K1-E11
Method BLASTX
NCBI GI g4510363
BLAST score 125
E value 6.0e-12
Match length 59
% identity 67
NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No. 224265
Seq. ID LIB3166-006-P1-K1-E2
Method BLASTX
NCBI GI g1351974
BLAST score 568
E value 1.0e-58
Match length 110
% identity 100
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir_S49325
ADP-ribosylation factor - maize >gi_1076789_pir_S53486
ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 224266
Seq. ID LIB3166-006-P1-K1-E3
Method BLASTX
NCBI GI g125606
BLAST score 463
E value 2.0e-46
Match length 99
% identity 88
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248
pyruvate kinase (EC 2.7.1.40) - potato
>gi_22576_emb_CAA37727_(X53688) pyruvate kinase [Solanum tuberosum]

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Seq. No. 224267
Seq. ID LIB3166-006-P1-K1-E4
Method BLASTX
NCBI GI g4102861
BLAST score 540
E value 2.0e-55
Match length 111
% identity 86
NCBI Description (AF016893) copper/zinc-superoxide dismutase [Populus tremuloides]

Seq. No. 224268
Seq. ID LIB3166-006-P1-K1-E6
Method BLASTX
NCBI GI g1895084
BLAST score 172
E value 3.0e-12
Match length 101
% identity 47
NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No. 224269
Seq. ID LIB3166-006-P1-K1-E7
Method BLASTX
NCBI GI g4263507
BLAST score 444
E value 3.0e-44
Match length 133
% identity 61
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224270
Seq. ID LIB3166-006-P1-K1-E8
Method BLASTX
NCBI GI g4220534
BLAST score 242
E value 2.0e-20
Match length 66
% identity 77
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 224271
Seq. ID LIB3166-006-P1-K1-E9
Method BLASTX
NCBI GI g4093157
BLAST score 204
E value 5.0e-16
Match length 93
% identity 56
NCBI Description (AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana]

Seq. No. 224272
Seq. ID LIB3166-006-P1-K1-F1
Method BLASTX
NCBI GI g1769903

BLAST score 482
E value 1.0e-48
Match length 124
% identity 73
NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No. 224273
Seq. ID LIB3166-006-P1-K1-F2
Method BLASTX
NCBI GI g1742961
BLAST score 169
E value 5.0e-12
Match length 99
% identity 48
NCBI Description (X94756) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No. 224274
Seq. ID LIB3166-006-P1-K1-F5
Method BLASTX
NCBI GI g1263291
BLAST score 511
E value 5.0e-52
Match length 115
% identity 80
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 224275
Seq. ID LIB3166-006-P1-K1-F6
Method BLASTX
NCBI GI g1531758
BLAST score 552
E value 4.0e-63
Match length 133
% identity 92
NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 224276
Seq. ID LIB3166-006-P1-K1-G1
Method BLASTX
NCBI GI g3901012
BLAST score 501
E value 6.0e-51
Match length 125
% identity 73
NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 224277
Seq. ID LIB3166-006-P1-K1-G2
Method BLASTX
NCBI GI g2462762
BLAST score 169
E value 2.0e-12
Match length 70
% identity 59

09624016-11010000

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 224278
Seq. ID LIB3166-006-P1-K1-G3
Method BLASTX
NCBI GI g1518540
BLAST score 428
E value 2.0e-42
Match length 95
% identity 84
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 224279
Seq. ID LIB3166-006-P1-K1-G4
Method BLASTX
NCBI GI g3668086
BLAST score 223
E value 3.0e-18
Match length 72
% identity 74
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 224280
Seq. ID LIB3166-006-P1-K1-G5
Method BLASTX
NCBI GI g2245131
BLAST score 304
E value 7.0e-28
Match length 125
% identity 50
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224281
Seq. ID LIB3166-006-P1-K1-G6
Method BLASTX
NCBI GI g4539348
BLAST score 167
E value 5.0e-12
Match length 56
% identity 55
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No. 224282
Seq. ID LIB3166-006-P1-K1-G7
Method BLASTX
NCBI GI g3915023
BLAST score 318
E value 9.0e-30
Match length 86
% identity 70
NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1
(UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1)
>gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No. 224283

Seq. ID LIB3166-006-P1-K1-H10
Method BLASTX
NCBI GI g2498731
BLAST score 318
E value 2.0e-29
Match length 84
% identity 68
NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
>gi_1362013_pir_S57611 zeta-crystallin homolog -
Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 224284
Seq. ID LIB3166-006-P1-K1-H3
Method BLASTX
NCBI GI g2443329
BLAST score 373
E value 6.0e-36
Match length 113
% identity 66
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 224285
Seq. ID LIB3166-006-P1-K1-H4
Method BLASTX
NCBI GI g3668089
BLAST score 302
E value 2.0e-27
Match length 104
% identity 51
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 224286
Seq. ID LIB3166-006-P1-K1-H7
Method BLASTX
NCBI GI g4263777
BLAST score 176
E value 8.0e-13
Match length 85
% identity 47
NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No. 224287
Seq. ID LIB3166-007-P1-K1-A12
Method BLASTX
NCBI GI g2497742
BLAST score 186
E value 6.0e-14
Match length 37
% identity 95
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
>gi_995907 (U15153) nonspecific lipid transfer protein
precursor [Gossypium hirsutum]

Seq. No. 224288

Seq. ID LIB3166-007-P1-K1-A2
Method BLASTX
NCBI GI g116923
BLAST score 172
E value 2.0e-12
Match length 102
% identity 44
NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
>gi_111414_pir_S13520 beta-COP protein - rat
>gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No. 224289
Seq. ID LIB3166-007-P1-K1-A3
Method BLASTX
NCBI GI g4158232
BLAST score 511
E value 4.0e-52
Match length 107
% identity 90
NCBI Description (Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No. 224290
Seq. ID LIB3166-007-P1-K1-A4
Method BLASTX
NCBI GI g4455364
BLAST score 304
E value 9.0e-28
Match length 107
% identity 54
NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No. 224291
Seq. ID LIB3166-007-P1-K1-A9
Method BLASTX
NCBI GI g3193287
BLAST score 275
E value 2.0e-24
Match length 104
% identity 54
NCBI Description (AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No. 224292
Seq. ID LIB3166-007-P1-K1-B1
Method BLASTX
NCBI GI g3128216
BLAST score 282
E value 3.0e-25
Match length 85
% identity 61
NCBI Description (AC004077) putative GA4 protein [Arabidopsis thaliana]

Seq. No. 224293
Seq. ID LIB3166-007-P1-K1-B11

Method BLASTX
NCBI GI g3046703
BLAST score 421
E value 4.0e-65
Match length 136
% identity 91
NCBI Description (AL021749) protein kinase ADK1-like protein [Arabidopsis thaliana]

Seq. No. 224294
Seq. ID LIB3166-007-P1-K1-B12
Method BLASTX
NCBI GI g3219353
BLAST score 453
E value 2.0e-47
Match length 135
% identity 73
NCBI Description (AF061514) manganese superoxide dismutase [Gossypium hirsutum]

Seq. No. 224295
Seq. ID LIB3166-007-P1-K1-B9
Method BLASTX
NCBI GI g4105696
BLAST score 275
E value 7.0e-25
Match length 57
% identity 93
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No. 224296
Seq. ID LIB3166-007-P1-K1-C1
Method BLASTX
NCBI GI g4049399
BLAST score 158
E value 1.0e-10
Match length 101
% identity 37
NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]

Seq. No. 224297
Seq. ID LIB3166-007-P1-K1-C11
Method BLASTX
NCBI GI g3738291
BLAST score 241
E value 2.0e-20
Match length 95
% identity 46
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 224298
Seq. ID LIB3166-007-P1-K1-C6
Method BLASTX
NCBI GI g2827634
BLAST score 163
E value 3.0e-11
Match length 91

% identity 43
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 224299
Seq. ID LIB3166-007-P1-K1-C7
Method BLASTX
NCBI GI g1418331
BLAST score 195
E value 6.0e-15
Match length 102
% identity 39
NCBI Description (X95909) receptor like protein kinase [Arabidopsis thaliana]

Seq. No. 224300
Seq. ID LIB3166-007-P1-K1-C8
Method BLASTX
NCBI GI g115833
BLAST score 163
E value 2.0e-16
Match length 94
% identity 57
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No. 224301
Seq. ID LIB3166-007-P1-K1-C9
Method BLASTX
NCBI GI g4210451
BLAST score 163
E value 5.0e-19
Match length 71
% identity 76
NCBI Description (AB016472) ARR2 protein [Arabidopsis thaliana]

Seq. No. 224302
Seq. ID LIB3166-007-P1-K1-D1
Method BLASTX
NCBI GI g120669
BLAST score 564
E value 3.0e-58
Match length 113
% identity 94
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 224303
Seq. ID LIB3166-007-P1-K1-D10
Method BLASTX
NCBI GI g541818
BLAST score 490
E value 1.0e-49

Match length 135
 % identity 71
 NCBI Description protein kinase - common ice plant (fragment)
 >gi_457693_emb_CAA82994_(Z30333) protein kinase
 [Mesembryanthemum crystallinum]

 Seq. No. 224304
 Seq. ID LIB3166-007-P1-K1-D12
 Method BLASTX
 NCBI GI g3522945
 BLAST score 183
 E value 1.0e-13
 Match length 95
 % identity 35
 NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

 Seq. No. 224305
 Seq. ID LIB3166-007-P1-K1-D3
 Method BLASTX
 NCBI GI g2407790
 BLAST score 414
 E value 1.0e-40
 Match length 115
 % identity 18
 NCBI Description (AF019910) grr1 [Glycine max]

 Seq. No. 224306
 Seq. ID LIB3166-007-P1-K1-D4
 Method BLASTX
 NCBI GI g3688123
 BLAST score 434
 E value 5.0e-43
 Match length 134
 % identity 66
 NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum majus]

 Seq. No. 224307
 Seq. ID LIB3166-007-P1-K1-D6
 Method BLASTX
 NCBI GI g4107323
 BLAST score 592
 E value 2.0e-61
 Match length 131
 % identity 86
 NCBI Description (AL035077) 60s ribosomal protein 110 [Schizosaccharomyces pombe]

 Seq. No. 224308
 Seq. ID LIB3166-007-P1-K1-D7
 Method BLASTX
 NCBI GI g464707
 BLAST score 560
 E value 9.0e-58
 Match length 114
 % identity 96
 NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal

protein S18.A - *Arabidopsis thaliana*
>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[*Arabidopsis thaliana*] >gi_434343_emb_CAA82273_ (Z28701)
S18 ribosomal protein [*Arabidopsis thaliana*]
>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[*Arabidopsis thaliana*] >gi_434906_emb_CAA82275_ (Z28962)
S18 ribosomal protein [*Arabidopsis thaliana*]
>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
[*Arabidopsis thaliana*] >gi_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
gb_R30430 come from this gene. [*Arabidopsis thaliana*]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
protein [*Arabidopsis thaliana*]

Seq. No. 224309
Seq. ID LIB3166-007-P1-K1-E1
Method BLASTX
NCBI GI g3128215
BLAST score 215
E value 3.0e-17
Match length 113
% identity 49
NCBI Description (AC004077) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 224310
Seq. ID LIB3166-007-P1-K1-E10
Method BLASTX
NCBI GI g3901014
BLAST score 235
E value 1.0e-19
Match length 55
% identity 76
NCBI Description (AJ130886) metallothionein-like protein class II [*Fagus sylvatica*]

Seq. No. 224311
Seq. ID LIB3166-007-P1-K1-E3
Method BLASTX
NCBI GI g2738949
BLAST score 488
E value 2.0e-49
Match length 99
% identity 93
NCBI Description (AF022213) cytosolic ascorbate peroxidase [*Fragaria x ananassa*]

Seq. No. 224312
Seq. ID LIB3166-007-P1-K1-E6
Method BLASTX
NCBI GI g3894183
BLAST score 264
E value 5.0e-23
Match length 109
% identity 31
NCBI Description (AC005662) calmodulin-like protein [*Arabidopsis thaliana*]

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Seq. No.	224313
Seq. ID	LIB3166-007-P1-K1-E7
Method	BLASTX
NCBI GI	g2558660
BLAST score	194
E value	8.0e-15
Match length	73
% identity	52
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.	224314
Seq. ID	LIB3166-007-P1-K1-E9
Method	BLASTX
NCBI GI	g462195
BLAST score	462
E value	3.0e-46
Match length	96
% identity	93
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir_S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]
Seq. No.	224315
Seq. ID	LIB3166-007-P1-K1-F12
Method	BLASTX
NCBI GI	g4098246
BLAST score	653
E value	1.0e-68
Match length	138
% identity	91
NCBI Description	(U76410) homeobox 2 protein [Lycopersicon esculentum]
Seq. No.	224316
Seq. ID	LIB3166-007-P1-K1-F2
Method	BLASTX
NCBI GI	g4163997
BLAST score	385
E value	3.0e-47
Match length	140
% identity	72
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]
Seq. No.	224317
Seq. ID	LIB3166-007-P1-K1-F5
Method	BLASTX
NCBI GI	g3250676
BLAST score	325
E value	1.0e-35
Match length	109
% identity	76
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]
Seq. No.	224318
Seq. ID	LIB3166-007-P1-K1-F6

Method BLASTX
NCBI GI g2760349
BLAST score 375
E value 4.0e-36
Match length 122
% identity 13
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]

Seq. No. 224319
Seq. ID LIB3166-007-P1-K1-F7
Method BLASTX
NCBI GI g3426038
BLAST score 478
E value 2.0e-49
Match length 135
% identity 29
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 224320
Seq. ID LIB3166-007-P1-K1-F9
Method BLASTX
NCBI GI g2443878
BLAST score 310
E value 2.0e-28
Match length 119
% identity 57
NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 224321
Seq. ID LIB3166-007-P1-K1-G1
Method BLASTX
NCBI GI 92160156
BLAST score 477
E value 6.0e-52
Match length 138
% identity 75
NCBI Description (AC000132) Strong similarity to *S. pombe* leucyl-tRNA synthetase (gb Z73100). [Arabidopsis thaliana]

Seq. No. 224322
Seq. ID LIB3166-007-P1-K1-G10
Method BLASTX
NCBI GI g3582342
BLAST score 226
E value 1.0e-18
Match length 126
% identity . . . 41
NCBI Description (AC005496) putative flavonol 3-o-glucosyltransferase
[Arabidopsis thaliana]

Seq. No. 224323
Seq. ID LIB3166-007-P1-K1-G12
Method BLASTX
NCBI GI g2058313
BLAST score 271
E value 7.0e-24
Match length 65

% identity 77
NCBI Description (X97433) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No. 224324
Seq. ID LIB3166-007-P1-K1-G4
Method BLASTX
NCBI GI g2464855
BLAST score 382
E value 2.0e-38
Match length 92
% identity 87
NCBI Description (Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No. 224325
Seq. ID LIB3166-007-P1-K1-G5
Method BLASTX
NCBI GI g3915037
BLAST score 621
E value 6.0e-65
Match length 132
% identity 91
NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
>gi_2570067_emb_CAA04512_ (AJ001071) second sucrose
synthase [Pisum sativum]

Seq. No. 224326
Seq. ID LIB3166-007-P1-K1-G6
Method BLASTX
NCBI GI g1703446
BLAST score 379
E value 1.0e-36
Match length 116
% identity 68
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
>gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
>gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
thaliana]

Seq. No. 224327
Seq. ID LIB3166-007-P1-K1-G7
Method BLASTX
NCBI GI g3264767
BLAST score 415
E value 9.0e-41
Match length 125
% identity 61
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 224328
Seq. ID LIB3166-007-P1-K1-H10
Method BLASTX
NCBI GI g3341685
BLAST score 205
E value 4.0e-16
Match length 102
% identity 49
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 224329
Seq. ID LIB3166-007-P1-K1-H11
Method BLASTX
NCBI GI g2224927
BLAST score 320
E value 4.0e-49
Match length 122
% identity 80
NCBI Description (AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]

Seq. No. 224330
Seq. ID LIB3166-007-P1-K1-H12
Method BLASTX
NCBI GI g2495365
BLAST score 399
E value 5.0e-39
Match length 112
% identity 73
NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf_1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No. 224331
Seq. ID LIB3166-007-P1-K1-H2
Method BLASTX
NCBI GI g4539292
BLAST score 475
E value 7.0e-48
Match length 103
% identity 84
NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 224332
Seq. ID LIB3166-007-P1-K1-H3
Method BLASTX
NCBI GI g2618721
BLAST score 150
E value 3.0e-10
Match length 41
% identity 76
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 224333
Seq. ID LIB3166-008-P1-K1-A11
Method BLASTX
NCBI GI g1621268
BLAST score 268
E value 9.0e-24
Match length 93
% identity 63
NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 224334
Seq. ID LIB3166-008-P1-K1-A12
Method BLASTX

NCBI GI g3281861
BLAST score 375
E value 4.0e-36
Match length 127
% identity 56
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 224335
Seq. ID LIB3166-008-P1-K1-A3
Method BLASTX
NCBI GI g3236253
BLAST score 569
E value 7.0e-59
Match length 129
% identity 81
NCBI Description (AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 224336
Seq. ID LIB3166-008-P1-K1-A7
Method BLASTX
NCBI GI g4234941
BLAST score 227
E value 3.0e-19
Match length 52
% identity 87
NCBI Description (AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No. 224337
Seq. ID LIB3166-008-P1-K1-B1
Method BLASTX
NCBI GI g1750376
BLAST score 531
E value 2.0e-54
Match length 119
% identity 83
NCBI Description (U80808) ubiquitin activating enzyme [Arabidopsis thaliana]
>gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1)
[Arabidopsis thaliana]

Seq. No. 224338
Seq. ID LIB3166-008-P1-K1-B12
Method BLASTX
NCBI GI g2979548
BLAST score 202
E value 5.0e-16
Match length 97
% identity 39
NCBI Description (AC003680) putative 7-ethoxycoumarin O-deethylase
[Arabidopsis thaliana]

Seq. No. 224339
Seq. ID LIB3166-008-P1-K1-B3
Method BLASTX
NCBI GI g478713
BLAST score 414

09634016-1010000

E value	1.0e-40
Match length	84
% identity	96
NCBI Description	AP1 protein - <i>Arabidopsis thaliana</i> >gi_383297_prf_1902329A APETALA1 gene [<i>Arabidopsis thaliana</i>]
Seq. No.	224340
Seq. ID	LIB3166-008-P1-K1-B4
Method	BLASTX
NCBI GI	g2618691
BLAST score	179
E value	4.0e-13
Match length	75
% identity	55
NCBI Description	(AC002510) putative chloroplast envelope Ca ²⁺ -ATPase [<i>Arabidopsis thaliana</i>]
Seq. No.	224341
Seq. ID	LIB3166-008-P1-K1-B7
Method	BLASTX
NCBI GI	g4510375
BLAST score	182
E value	8.0e-14
Match length	72
% identity	58
NCBI Description	(AC007017) putative homeotic protein BELL [<i>Arabidopsis thaliana</i>]
Seq. No.	224342
Seq. ID	LIB3166-008-P1-K1-C10
Method	BLASTX
NCBI GI	g2959781
BLAST score	480
E value	2.0e-48
Match length	106
% identity	86
NCBI Description	(AJ223508) Zwiller protein [<i>Arabidopsis thaliana</i>]
Seq. No.	224343
Seq. ID	LIB3166-008-P1-K1-C3
Method	BLASTX
NCBI GI	g3927836
BLAST score	341
E value	4.0e-32
Match length	114
% identity	62
NCBI Description	(AC005727) unknown protein [<i>Arabidopsis thaliana</i>]
Seq. No.	224344
Seq. ID	LIB3166-008-P1-K1-C4
Method	BLASTX
NCBI GI	g4220480
BLAST score	279
E value	8.0e-25
Match length	119
% identity	50
NCBI Description	(AC006069) unknown protein [<i>Arabidopsis thaliana</i>]

093640-1101000

Seq. No. 224345
Seq. ID LIB3166-008-P1-K1-C5
Method BLASTX
NCBI GI g2833386
BLAST score 275
E value 2.0e-24
Match length 81
% identity 74
NCBI Description RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR
(PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E)
>gi_2129493_pir_S62724 ribulose-phosphate 3-epimerase (EC
5.1.3.1) precursor - spinach >gi_1162980 (L42328)
ribulose-5-phosphate 3-epimerase [Spinacia oleracea]
>gi_3264788 (AF070941) ribulose-phosphate 3-epimerase
[Spinacia oleracea] >gi_1587969_prf_2207382A
D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No. 224346
Seq. ID LIB3166-008-P1-K1-C9
Method BLASTX
NCBI GI g3367568
BLAST score 429
E value 2.0e-42
Match length 117
% identity 70
NCBI Description (AL031135) protein kinase - like protein [Arabidopsis
thaliana]

Seq. No. 224347
Seq. ID LIB3166-008-P1-K1-D10
Method BLASTX
NCBI GI g3378430
BLAST score 188
E value 1.0e-14
Match length 61
% identity 66
NCBI Description (AF079317) semialdehyde dehydrogenase [Sphingomonas
aromaticivorans]

Seq. No. 224348
Seq. ID LIB3166-008-P1-K1-D11
Method BLASTX
NCBI GI g2463569
BLAST score 343
E value 2.0e-32
Match length 73
% identity 86
NCBI Description (AB007503) squalene synthase [Glycine max]

Seq. No. 224349
Seq. ID LIB3166-008-P1-K1-D12
Method BLASTX
NCBI GI g2443881
BLAST score 163
E value 3.0e-11
Match length 77

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% identity 28
NCBI Description (AC002294) contains beta-transducin motif [Arabidopsis thaliana]

Seq. No. 224350
Seq. ID LIB3166-008-P1-K1-D4
Method BLASTX
NCBI GI g2911043
BLAST score 234
E value 1.0e-19
Match length 106
% identity 53
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 224351
Seq. ID LIB3166-008-P1-K1-D5
Method BLASTX
NCBI GI g3582333
BLAST score 587
E value 6.0e-61
Match length 131
% identity 79
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224352
Seq. ID LIB3166-008-P1-K1-D6
Method BLASTX
NCBI GI g3986750
BLAST score 226
E value 8.0e-19
Match length 50
% identity 86
NCBI Description (AF107464) serine/threonine protein phosphatase type 2A [Hevea brasiliensis]

Seq. No. 224353
Seq. ID LIB3166-008-P1-K1-E6
Method BLASTX
NCBI GI g4574320
BLAST score 106
E value 1.0e-08
Match length 59
% identity 63
NCBI Description (AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]

Seq. No. 224354
Seq. ID LIB3166-008-P1-K1-E9
Method BLASTX
NCBI GI g4510376
BLAST score 331
E value 6.0e-31
Match length 122
% identity 54
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 224355

Seq. ID LIB3166-008-P1-K1-F1
Method BLASTX
NCBI GI g2129915
BLAST score 330
E value 8.0e-31
Match length 115
% identity 57
NCBI Description ferredoxin precursor - sweet orange
>gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic
ferredoxin [Citrus sinensis]

Seq. No. 224356
Seq. ID LIB3166-008-P1-K1-F11
Method BLASTX
NCBI GI g2501850
BLAST score 507
E value 1.0e-51
Match length 102
% identity 92
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No. 224357
Seq. ID LIB3166-008-P1-K1-F3
Method BLASTX
NCBI GI g3033400
BLAST score 284
E value 7.0e-26
Match length 91
% identity 69
NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 224358
Seq. ID LIB3166-008-P1-K1-F4
Method BLASTX
NCBI GI g2809246
BLAST score 203
E value 6.0e-16
Match length 64
% identity 55
NCBI Description (AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No. 224359
Seq. ID LIB3166-008-P1-K1-F6
Method BLASTX
NCBI GI g4432842
BLAST score 204
E value 5.0e-16
Match length 135
% identity 39
NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224360
Seq. ID LIB3166-008-P1-K1-F7
Method BLASTX
NCBI GI g417073
BLAST score 472

E value 2.0e-47
 Match length 118
 % identity 75
 NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
 >gi_484529_pir_JQ1977 glutamate synthase (NADH) (EC
 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate
 synthase [Medicago sativa]

 Seq. No. 224361
 Seq. ID LIB3166-008-P1-K1-F8
 Method BLASTX
 NCBI GI g417073
 BLAST score 140
 E value 4.0e-09
 Match length 39
 % identity 64
 NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
 >gi_484529_pir_JQ1977 glutamate synthase (NADH) (EC
 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate
 synthase [Medicago sativa]

 Seq. No. 224362
 Seq. ID LIB3166-008-P1-K1-G12
 Method BLASTX
 NCBI GI g1168734
 BLAST score 258
 E value 7.0e-31
 Match length 106
 % identity 71
 NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD)
 >gi_288753_emb_CAA79622 (Z19568) cinnamyl alcohol
 dehydrogenase [Populus deltoides]

 Seq. No. 224363
 Seq. ID LIB3166-008-P1-K1-G2
 Method BLASTX
 NCBI GI g3142300
 BLAST score 508
 E value 1.0e-51
 Match length 121
 % identity 81
 NCBI Description (AC002411) Contains similarity to pre-mRNA processing
 protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
 and gb_T88158, gb_N38703 and gb_AA651043 come from this
 gene. [Arabidopsis thaliana]

 Seq. No. 224364
 Seq. ID LIB3166-008-P1-K1-G3
 Method BLASTX
 NCBI GI g4376592
 BLAST score 163
 E value 3.0e-11
 Match length 121
 % identity 11
 NCBI Description (AE001616) S1 Ribosomal Protein [Chlamydia pneumoniae]

 Seq. No. 224365

Seq. ID LIB3166-008-P1-K1-G4
 Method BLASTX
 NCBI GI g2224733
 BLAST score 171
 E value 4.0e-12
 Match length 91
 % identity 51
 NCBI Description (AB004933) Aux22e [Vigna radiata]

Seq. No. 224366
 Seq. ID LIB3166-008-P1-K1-G7
 Method BLASTX
 NCBI GI g1220196
 BLAST score 279
 E value 8.0e-31
 Match length 104
 % identity 70
 NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 224367
 Seq. ID LIB3166-008-P1-K1-G9
 Method BLASTX
 NCBI GI g4220538
 BLAST score 416
 E value 5.0e-41
 Match length 101
 % identity 80
 NCBI Description (AL035356) NADPH-ferrihemoprotein reductase ATR1 [Arabidopsis thaliana]

Seq. No. 224368
 Seq. ID LIB3166-008-P1-K1-H1
 Method BLASTX
 NCBI GI g4580460
 BLAST score 431
 E value 1.0e-42
 Match length 114
 % identity 79
 NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No. 224369
 Seq. ID LIB3166-008-P1-K1-H2
 Method BLASTX
 NCBI GI g3549667
 BLAST score 554
 E value 4.0e-57
 Match length 121
 % identity 87
 NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No. 224370
 Seq. ID LIB3166-008-P1-K1-H9
 Method BLASTX
 NCBI GI g1657382
 BLAST score 497

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E value 4.0e-52
Match length 117
% identity 86
NCBI Description (Y09101) cholinephosphate cytidylyltransferase [Pisum sativum]

Seq. No. 224371
Seq. ID LIB3166-009-P1-K1-A7
Method BLASTX
NCBI GI g2119278
BLAST score 622
E value 5.0e-65
Match length 141
% identity 87
NCBI Description tubulin beta-1 chain - rice

Seq. No. 224372
Seq. ID LIB3166-009-P1-K1-B10
Method BLASTX
NCBI GI g462147
BLAST score 258
E value 2.0e-22
Match length 71
% identity 69
NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
(PHI) >gi_541866_pir_S41808 glucose-6-phosphate isomerase
(EC 5.3.1.9) - Arabidopsis thaliana
>gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 224373
Seq. ID LIB3166-009-P1-K1-B3
Method BLASTX
NCBI GI g2252839
BLAST score 447
E value 2.0e-44
Match length 142
% identity 59
NCBI Description (AF013293) Similar to receptor-like protein kinase precursor [Arabidopsis thaliana]

Seq. No. 224374
Seq. ID LIB3166-009-P1-K1-B4
Method BLASTX
NCBI GI g421941
BLAST score 326
E value 3.0e-30
Match length 70
% identity 90
NCBI Description GTP-binding protein, ras-related - common tobacco
>gi_296878_emb_CAA50609_ (X71609) ras-related GTP-binding protein [Nicotiana tabacum]

Seq. No. 224375
Seq. ID LIB3166-009-P1-K1-B6
Method BLASTX

NCBI GI g115833
BLAST score 529
E value 4.0e-54
Match length 129
% identity 78
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No. 224376
Seq. ID LIB3166-009-P1-K1-C1
Method BLASTX
NCBI GI g1702983
BLAST score 325
E value 3.0e-30
Match length 110
% identity 56
NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir_S11850 hypothetical protein - garden strawberry >gi_22573_emb_CAA36676 (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein [Fragaria ananassa]

Seq. No. 224377
Seq. ID LIB3166-009-P1-K1-C11
Method BLASTX
NCBI GI g3395427
BLAST score 169
E value 6.0e-12
Match length 103
% identity 36
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 224378
Seq. ID LIB3166-009-P1-K1-C3
Method BLASTX
NCBI GI g1943751
BLAST score 624
E value 3.0e-65
Match length 141
% identity 89
NCBI Description (U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca²⁺-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No. 224379
Seq. ID LIB3166-009-P1-K1-C6
Method BLASTX
NCBI GI g2245066
BLAST score 402
E value 3.0e-39
Match length 134
% identity 62
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 224380

Seq. ID LIB3166-009-P1-K1-C7
Method BLASTX
NCBI GI g3608137
BLAST score 182
E value 2.0e-13
Match length 79
% identity 49
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 224381
Seq. ID LIB3166-009-P1-K1-D2
Method BLASTX
NCBI GI g2632254
BLAST score 371
E value 1.0e-35
Match length 102
% identity 70
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 224382
Seq. ID LIB3166-009-P1-K1-D6
Method BLASTX
NCBI GI g1944216
BLAST score 275
E value 7.0e-25
Match length 97
% identity 67
NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 224383
Seq. ID LIB3166-009-P1-K1-D8
Method BLASTX
NCBI GI g541847
BLAST score 542
E value 1.0e-55
Match length 120
% identity 84
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - *Arabidopsis thaliana*

Seq. No. 224384
Seq. ID LIB3166-009-P1-K1-E12
Method BLASTX
NCBI GI g1403522
BLAST score 336
E value 2.0e-31
Match length 107
% identity 62
NCBI Description (X57187) chitinase [Phaseolus vulgaris]

Seq. No. 224385
Seq. ID LIB3166-009-P1-K1-E2
Method BLASTX
NCBI GI g4490297
BLAST score 279
E. value 8.0e-25
Match length 120
% identity 55

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NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]
Seq. No.	224386
Seq. ID	LIB3166-009-P1-K1-E3
Method	BLASTX
NCBI GI	g3287691
BLAST score	318
E value	2.0e-29
Match length	126
% identity	54
NCBI Description	(AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]
Seq. No.	224387
Seq. ID	LIB3166-009-P1-K1-E4
Method	BLASTX
NCBI GI	g1871192
BLAST score	344
E value	2.0e-32
Match length	137
% identity	57
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]
Seq. No.	224388
Seq. ID	LIB3166-009-P1-K1-E6
Method	BLASTX
NCBI GI	g2708750
BLAST score	382
E value	7.0e-37
Match length	134
% identity	56
NCBI Description	(AC003952) putative physical impedance protein [Arabidopsis thaliana]
Seq. No.	224389
Seq. ID	LIB3166-009-P1-K1-E7
Method	BLASTX
NCBI GI	g115833
BLAST score	412
E value	2.0e-40
Match length	108
% identity	75
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]
Seq. No.	224390
Seq. ID	LIB3166-009-P1-K1-F11
Method	BLASTX
NCBI GI	g4545262
BLAST score	215
E value	3.0e-17
Match length	48
% identity	85
NCBI Description	(AF118230) metallothionein-like protein [Gossypium

hirsutum]

Seq. No. 224391
Seq. ID LIB3166-009-P1-K1-F12
Method BLASTX
NCBI GI g4099482
BLAST score 266
E value 3.0e-23
Match length 127
% identity 46
NCBI Description (U87791) eRFS [Homo sapiens]

Seq. No. 224392
Seq. ID LIB3166-009-P1-K1-F2
Method BLASTX
NCBI GI g541847
BLAST score 268
E value 7.0e-24
Match length 63
% identity 76
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

Seq. No. 224393
Seq. ID LIB3166-009-P1-K1-F3
Method BLASTX
NCBI GI g1707944
BLAST score 635
E value 1.0e-66
Match length 137
% identity 93
NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT PRECURSOR 2 (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_541976_pir_S41292 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - fava bean >gi_440595_emb_CAA54260_ (X76941) ADP-glucose pyrophosphorylase [Vicia faba]

Seq. No. 224394
Seq. ID LIB3166-009-P1-K1-F4
Method BLASTX
NCBI GI g4335750
BLAST score 164
E value 7.0e-12
Match length 57
% identity 58
NCBI Description (AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No. 224395
Seq. ID LIB3166-009-P1-K1-F7
Method BLASTX
NCBI GI g3023536
BLAST score 388
E value 1.0e-37
Match length 127
% identity 58

NCBI Description MADS BOX PROTEIN CMB1 >gi_695317 (L40404) MADS box protein [Dianthus caryophyllus]

Seq. No. 224396
Seq. ID LIB3166-009-P1-K1-F9
Method BLASTX
NCBI GI g1345698
BLAST score 715
E value 6.0e-76
Match length 135
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi_99601_pir_S20917 chlorophyll a/b-binding protein - upland cotton >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding protein [Gossypium hirsutum]

Seq. No. 224397
Seq. ID LIB3166-009-P1-K1-G10
Method BLASTX
NCBI GI g464707
BLAST score 535
E value 6.0e-55
Match length 114
% identity 90
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. 224398
Seq. ID LIB3166-009-P1-K1-G11
Method BLASTX
NCBI GI g3176726
BLAST score 409
E value 4.0e-44
Match length 124
% identity 75
NCBI Description (AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No. 224399
Seq. ID LIB3166-009-P1-K1-G2
Method BLASTX
NCBI GI g2244749
BLAST score 616

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E value 3.0e-64
Match length 128
% identity 91
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 224400
Seq. ID LIB3166-009-P1-K1-G3
Method BLASTX
NCBI GI g2109293
BLAST score 509
E value 9.0e-52
Match length 121
% identity 85
NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 224401
Seq. ID LIB3166-009-P1-K1-G4
Method BLASTX
NCBI GI g1708236
BLAST score 476
E value 5.0e-48
Match length 118
% identity 78
NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
>gi_2129617_pir_JC4567 hydroxymethylglutaryl-CoA synthase
(EC 4.1.3.5) - Arabidopsis thaliana
>gi_1143390_emb_CAA58763 (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
>gi_1586548_prf_2204245A hydroxy methylglutaryl CoA
synthase [Arabidopsis thaliana]

Seq. No. 224402
Seq. ID LIB3166-009-P1-K1-G5
Method BLASTX
NCBI GI g3334659
BLAST score 309
E value 2.0e-28
Match length 134
% identity 52
NCBI Description (Y10489) putative cytochrome P450 [Glycine max]

Seq. No. 224403
Seq. ID LIB3166-009-P1-K1-H2
Method BLASTX
NCBI GI g3763933
BLAST score 277
E value 1.0e-24
Match length 127
% identity 44
NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 224404
Seq. ID LIB3166-009-P1-K1-H6
Method BLASTX
NCBI GI g441457

BLAST score 462
E value 3.0e-46
Match length 92
% identity 93
NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No. 224405
Seq. ID LIB3166-009-P1-K1-H8
Method BLASTX
NCBI GI g1946267
BLAST score 211
E value 8.0e-17
Match length 60
% identity 65
NCBI Description (Y11415) myb [Oryza sativa]

Seq. No. 224406
Seq. ID LIB3166-010-P1-K1-A1
Method BLASTX
NCBI GI g2827002
BLAST score 220
E value 2.0e-18
Match length 42
% identity 100
NCBI Description (AF005993) HSP70 [Triticum aestivum]

Seq. No. 224407
Seq. ID LIB3166-010-P1-K1-A10
Method BLASTX
NCBI GI g4580392
BLAST score 283
E value 3.0e-25
Match length 123
% identity 46
NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224408
Seq. ID LIB3166-010-P1-K1-A11
Method BLASTX
NCBI GI g1399917
BLAST score 156
E value 2.0e-10
Match length 79
% identity 41
NCBI Description (U60144) replication factor C large subunit [Anas platyrhynchos]

Seq. No. 224409
Seq. ID LIB3166-010-P1-K1-A3
Method BLASTX
NCBI GI g1944216
BLAST score 329
E value 3.0e-31
Match length 72
% identity 85
NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]

09/01/2010

Seq. No. 224410
Seq. ID LIB3166-010-P1-K1-A8
Method BLASTX
NCBI GI g1169586
BLAST score 213
E value 1.0e-17
Match length 61
% identity 70
NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
(CY-F1) >gi_542079_pir_S41287 fructose-bisphosphatase (EC
3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946)
fructose-1,6-bisphosphatase [Solanum tuberosum]

Seq. No. 224411
Seq. ID LIB3166-010-P1-K1-A9
Method BLASTX
NCBI GI g289920
BLAST score 373
E value 4.0e-36
Match length 89
% identity 82
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
hirsutum]

Seq. No. 224412
Seq. ID LIB3166-010-P1-K1-B10
Method BLASTX
NCBI GI g19464
BLAST score 329
E value 1.0e-30
Match length 85
% identity 62
NCBI Description (X54464) ribulose bisphosphate carboxylase [Larix
laricina]

Seq. No. 224413
Seq. ID LIB3166-010-P1-K1-B11
Method BLASTX
NCBI GI g231806
BLAST score 267
E value 2.0e-36
Match length 102
% identity 83
NCBI Description CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE)
>gi_322681_pir_S29556 naringenin-chalcone synthase (EC
2.3.1.74) - apple tree (fragment) >gi_19589_emb_CAA48773_
(X68977) naregenin-chalcone synthase [Malus sp.]

Seq. No. 224414
Seq. ID LIB3166-010-P1-K1-B2
Method BLASTX
NCBI GI g1173256
BLAST score 298
E value 2.0e-27
Match length 68

% identity 84
 NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_(X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No. 224415
 Seq. ID LIB3166-010-P1-K1-B3
 Method BLASTX
 NCBI GI g218179
 BLAST score 183
 E value 7.0e-21
 Match length 92
 % identity 59
 NCBI Description (D10207) H-ATPase [Oryza sativa] >gi_444339_prf_1906387A H-ATPase [Oryza sativa]

Seq. No. 224416
 Seq. ID LIB3166-010-P1-K1-B7
 Method BLASTX
 NCBI GI g2129655
 BLAST score 192
 E value 1.0e-14
 Match length 71
 % identity 58
 NCBI Description OBP32pep protein - Arabidopsis thaliana (fragment) >gi_1022799 (U37698) OBP32pep [Arabidopsis thaliana]

Seq. No. 224417
 Seq. ID LIB3166-010-P1-K1-B8
 Method BLASTX
 NCBI GI g3955021
 BLAST score 381
 E value 1.0e-36
 Match length 103
 % identity 73
 NCBI Description (AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No. 224418
 Seq. ID LIB3166-010-P1-K1-C10
 Method BLASTX
 NCBI GI g125578
 BLAST score 562
 E value 5.0e-58
 Match length 116
 % identity 93
 NCBI Description PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_167266 (M73707) phosphoribulokinase [Mesembryanthemum crystallinum]

Seq. No. 224419
 Seq. ID LIB3166-010-P1-K1-C11
 Method BLASTX
 NCBI GI g4558547
 BLAST score 277
 E value 1.0e-24

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Match length 141
% identity 45
NCBI Description (AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224420
Seq. ID LIB3166-010-P1-K1-C12
Method BLASTX
NCBI GI g3834303
BLAST score 428
E value 3.0e-42
Match length 138
% identity 63
NCBI Description (AC005679) F9K20.3 [Arabidopsis thaliana]

Seq. No. 224421
Seq. ID LIB3166-010-P1-K1-C4
Method BLASTX
NCBI GI g543905
BLAST score 500
E value 1.0e-50
Match length 107
% identity 86
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
brassinosteroid-regulated protein [Glycine max]

Seq. No. 224422
Seq. ID LIB3166-010-P1-K1-C8
Method BLASTX
NCBI GI g3482973
BLAST score 429
E value 2.0e-42
Match length 127
% identity 71
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 224423
Seq. ID LIB3166-010-P1-K1-D1
Method BLASTX
NCBI GI g2980773
BLAST score 234
E value 1.0e-19
Match length 79
% identity 45
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 224424
Seq. ID LIB3166-010-P1-K1-D11
Method BLASTX
NCBI GI g4220533
BLAST score 378
E value 2.0e-36
Match length 127
% identity 34
NCBI Description (AL035356) putative mitochondrial uncoupling protein
[Arabidopsis thaliana]

Seq. No. 224425

Seq. ID LIB3166-010-P1-K1-D4
Method BLASTX
NCBI GI g4454009
BLAST score 154
E value 4.0e-10
Match length 95
% identity 40
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 224426
Seq. ID LIB3166-010-P1-K1-D7
Method BLASTX
NCBI GI g1621268
BLAST score 250
E value 1.0e-21
Match length 85
% identity 64
NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 224427
Seq. ID LIB3166-010-P1-K1-D9
Method BLASTX
NCBI GI g2982251
BLAST score 290
E value 4.0e-26
Match length 76
% identity 71
NCBI Description (AF051208) putative RNA-binding protein [Picea mariana]

Seq. No. 224428
Seq. ID LIB3166-010-P1-K1-E12
Method BLASTX
NCBI GI g2129825
BLAST score 540
E value 2.0e-57
Match length 139
% identity 83
NCBI Description dynamin-like protein phragmoplastin 12 - soybean
>gi_1217994 (U25547) SDL [Glycine max]

Seq. No. 224429
Seq. ID LIB3166-010-P1-K1-E2
Method BLASTX
NCBI GI g4580389
BLAST score 272
E value 5.0e-24
Match length 109
% identity 56
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 224430
Seq. ID LIB3166-010-P1-K1-E3
Method BLASTX
NCBI GI g1944216
BLAST score 358
E value 2.0e-34
Match length 80

% identity 85
NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 224431
Seq. ID LIB3166-010-P1-K1-E4
Method BLASTX
NCBI GI g1871192
BLAST score 148
E value 1.0e-09
Match length 64
% identity 47
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 224432
Seq. ID LIB3166-010-P1-K1-E6
Method BLASTX
NCBI GI g4545262
BLAST score 232
E value 3.0e-19
Match length 44
% identity 98
NCBI Description (AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No. 224433
Seq. ID LIB3166-010-P1-K1-E7
Method BLASTX
NCBI GI g4415913
BLAST score 302
E value 2.0e-27
Match length 122
% identity 61
NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 224434
Seq. ID LIB3166-010-P1-K1-F10
Method BLASTX
NCBI GI g3250675
BLAST score 253
E value 3.0e-22
Match length 75
% identity 67
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 224435
Seq. ID LIB3166-010-P1-K1-F12
Method BLASTX
NCBI GI g3297818
BLAST score 373
E value 8.0e-36
Match length 104
% identity 63
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 224436
Seq. ID LIB3166-010-P1-K1-F3

Method BLASTX
NCBI GI g4049410
BLAST score 419
E value 3.0e-41
Match length 118
% identity 66
NCBI Description (Y10225) L-ascorbate oxidase [Cucumis melo]

Seq. No. 224437
Seq. ID LIB3166-010-P1-K1-F6
Method BLASTX
NCBI GI g3885338
BLAST score 324
E value 3.0e-30
Match length 102
% identity 61
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 224438
Seq. ID LIB3166-010-P1-K1-F7
Method BLASTX
NCBI GI g116923
BLAST score 251
E value 1.0e-21
Match length 82
% identity 61
NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
>gi_111414_pir_S13520 beta-COP protein - rat
>gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No. 224439
Seq. ID LIB3166-010-P1-K1-F8
Method BLASTX
NCBI GI g1495804
BLAST score 657
E value 4.0e-69
Match length 142
% identity 85
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No. 224440
Seq. ID LIB3166-010-P1-K1-G1
Method BLASTX
NCBI GI g1707955
BLAST score 628
E value 9.0e-66
Match length 125
% identity 92
NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1
(GLUTAMATE--AMMONIA LIGASE) >gi_1134896_emb_CAA63981_
(X94320) glutamine synthetase [Vitis vinifera]

Seq. No. 224441
Seq. ID LIB3166-010-P1-K1-G10
Method BLASTX
NCBI GI g2935416

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BLAST score 554
E value 5.0e-57
Match length 139
% identity 78
NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]

Seq. No. 224442
Seq. ID LIB3166-010-P1-K1-G12
Method BLASTX
NCBI GI g2408068
BLAST score 241
E value 2.0e-20
Match length 107
% identity 42
NCBI Description (Z99165) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 224443
Seq. ID LIB3166-010-P1-K1-G2
Method BLASTX
NCBI GI g2370312
BLAST score 399
E value 7.0e-39
Match length 139
% identity 58
NCBI Description (AJ000995) DnaJ-like protein [Medicago sativa] >gi_3202020
(AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

Seq. No. 224444
Seq. ID LIB3166-010-P1-K1-G7
Method BLASTX
NCBI GI g2352492
BLAST score 190
E value 1.0e-14
Match length 68
% identity 59
NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No. 224445
Seq. ID LIB3166-010-P1-K1-H4
Method BLASTX
NCBI GI g4417267
BLAST score 261
E value 1.0e-22
Match length 132
% identity 39
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224446
Seq. ID LIB3166-010-P1-K1-H7
Method BLASTX
NCBI GI g116923
BLAST score 273
E value 4.0e-24
Match length 110
% identity 43

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NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir_S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]
Seq. No.	224447
Seq. ID	LIB3166-010-P1-K1-H9
Method	BLASTX
NCBI GI	g3935176
BLAST score	173
E value	2.0e-12
Match length	71
% identity	54
NCBI Description	(AC004557) F17L21.19 [Arabidopsis thaliana]
Seq. No.	224448
Seq. ID	LIB3166-011-P1-K1-A1
Method	BLASTX
NCBI GI	g4469023
BLAST score	323
E value	6.0e-30
Match length	98
% identity	68
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	224449
Seq. ID	LIB3166-011-P1-K1-A12
Method	BLASTX
NCBI GI	g3212869
BLAST score	495
E value	3.0e-50
Match length	120
% identity	74
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	224450
Seq. ID	LIB3166-011-P1-K1-A4
Method	BLASTX
NCBI GI	g2632252
BLAST score	271
E value	7.0e-24
Match length	134
% identity	46
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.	224451
Seq. ID	LIB3166-011-P1-K1-A5
Method	BLASTX
NCBI GI	g4544443
BLAST score	169
E value	5.0e-12
Match length	36
% identity	92
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]
Seq. No.	224452

096284016401000

Seq. ID	LIB3166-011-P1-K1-A8
Method	BLASTX
NCBI GI	g3702332
BLAST score	176
E value	9.0e-13
Match length	124
% identity	27
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	224453
Seq. ID	LIB3166-011-P1-K1-B1
Method	BLASTX
NCBI GI	g2129769
BLAST score	497
E value	2.0e-50
Match length	112
% identity	81
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]
Seq. No.	224454
Seq. ID	LIB3166-011-P1-K1-B10
Method	BLASTX
NCBI GI	g4455214
BLAST score	577
E value	8.0e-60
Match length	126
% identity	89
NCBI Description	(AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]
Seq. No.	224455
Seq. ID	LIB3166-011-P1-K1-B4
Method	BLASTX
NCBI GI	g2894612
BLAST score	485
E value	6.0e-49
Match length	112
% identity	79
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	224456
Seq. ID	LIB3166-011-P1-K1-B6
Method	BLASTX
NCBI GI	g485742
BLAST score	569
E value	7.0e-59
Match length	125
% identity	86
NCBI Description	(L32791) pyrophosphatase [Beta vulgaris]
Seq. No.	224457
Seq. ID	LIB3166-011-P1-K1-B8
Method	BLASTX
NCBI GI	g2129759
BLAST score	209

E value 1.0e-16
Match length 79
% identity 54
NCBI Description UDPglucose 4-epimerase (EC 5.1.3.2) - *Arabidopsis thaliana*
>gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate
glucose epimerase [*Arabidopsis thaliana*]

Seq. No. 224458
Seq. ID LIB3166-011-P1-K1-C1
Method BLASTX
NCBI GI g4539405
BLAST score 546
E value 4.0e-56
Match length 127
% identity 82
NCBI Description (AL049524) putative ribosomal protein L9, cytosolic
[Arabidopsis thaliana]

Seq. No. 224459
Seq. ID LIB3166-011-P1-K1-C10
Method BLASTX
NCBI GI g1871577
BLAST score 383
E value 5.0e-37
Match length 106
% identity 67
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No. 224460
Seq. ID LIB3166-011-P1-K1-C11
Method BLASTX
NCBI GI g322750
BLAST score 546
E value 4.0e-56
Match length 109
% identity 99
NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco
>gi_170217 (M74100) ubiquitin fusion protein [Nicotiana
sylvestris]

Seq. No. 224461
Seq. ID LIB3166-011-P1-K1-C12
Method BLASTX
NCBI GI g461942
BLAST score 525
E value 1.0e-53
Match length 135
% identity 74
NCBI Description DNAJ PROTEIN HOMOLOG 1 (DNAJ-1) >gi_479277_pir_S33312 dnaJ protein - leek (fragment) >gi_16087_emb_CAA492II_ (X69436) DNA J protein [Allium porrum] >gi_447267_prf_1914140A DnaJ protein [Allium porrum]

Seq. No. 224462
Seq. ID LIB3166-011-P1-K1-C2
Method BLASTX
NCBI GI g409756

BLAST score 146
 E value 2.0e-09
 Match length 88
 % identity 30
 NCBI Description (L25643) ATP/GTP nucleotide-binding protein [Leishmania infantum]

Seq. No. 224463
 Seq. ID LIB3166-011-P1-K1-C3
 Method BLASTX
 NCBI GI g1142621
 BLAST score 165
 E value 3.0e-16
 Match length 73
 % identity 67
 NCBI Description (U18349) phaseolin G-box binding protein PG2 [Phaseolus vulgaris]

Seq. No. 224464
 Seq. ID LIB3166-011-P1-K1-C4
 Method BLASTX
 NCBI GI g4262239
 BLAST score 273
 E value 4.0e-24
 Match length 133
 % identity 43
 NCBI Description (AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No. 224465
 Seq. ID LIB3166-011-P1-K1-C8
 Method BLASTX
 NCBI GI g3335060
 BLAST score 418
 E value 4.0e-41
 Match length 95
 % identity 88
 NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No. 224466
 Seq. ID LIB3166-011-P1-K1-C9
 Method BLASTX
 NCBI GI g464707
 BLAST score 538
 E value 3.0e-55
 Match length 110
 % identity 95
 NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal protein S18.A - Arabidopsis thaliana
 >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana]
 >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]

>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. 224467
Seq. ID LIB3166-011-P1-K1-D12
Method BLASTX
NCBI GI g1071913
BLAST score 421
E value 2.0e-41
Match length 109
% identity 78
NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No. 224468
Seq. ID LIB3166-011-P1-K1-D4
Method BLASTX
NCBI GI g2262170
BLAST score 211
E value 7.0e-17
Match length 114
% identity 47
NCBI Description (AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No. 224469
Seq. ID LIB3166-011-P1-K1-D5
Method BLASTX
NCBI GI g4455364
BLAST score 428
E value 3.0e-42
Match length 121
% identity 65
NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No. 224470
Seq. ID LIB3166-011-P1-K1-D6
Method BLASTX
NCBI GI g2500378
BLAST score 416
E value 7.0e-41
Match length 83
% identity 90
NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 224471
Seq. ID LIB3166-011-P1-K1-E10
Method BLASTX
NCBI GI g1174592
BLAST score 608

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E value 2.0e-63
Match length 113
% identity 99
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
- garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
sativum]

Seq. No. 224472
Seq. ID LIB3166-011-P1-K1-E11
Method BLASTX
NCBI GI g2052379
BLAST score 169
E value 3.0e-12
Match length 35
% identity 86
NCBI Description (U66343) calreticulin [Arabidopsis thaliana]

Seq. No. 224473
Seq. ID LIB3166-011-P1-K1-E2
Method BLASTX
NCBI GI g3080400
BLAST score 302
E value 2.0e-35
Match length 119
% identity 65
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
>gi_4455264_emb_CAB36800.1_ (AL035527) putative protein
[Arabidopsis thaliana]

Seq. No. 224474
Seq. ID LIB3166-011-P1-K1-E3
Method BLASTX
NCBI GI g2292917
BLAST score 258
E value 2.0e-22
Match length 84
% identity 64
NCBI Description (X99851) galactokinase [Arabidopsis thaliana]

Seq. No. 224475
Seq. ID LIB3166-011-P1-K1-E5
Method BLASTX
NCBI GI g128194
BLAST score 462
E value 2.0e-46
Match length 113
% identity 80
NCBI Description NITRATE REDUCTASE (NR) >gi_81572_pir_A41667 nitrate
reductase (NADH) (EC 1.6.6.1) - winter squash >gi_167499
(M33154) nitrate reductase [Cucurbita maxima]

Seq. No. 224476
Seq. ID LIB3166-011-P1-K1-E7
Method BLASTX
NCBI GI g3036807
BLAST score 324
E value 4.0e-30

Document ID: 00000000000000000000000000000000

Match length 88
% identity 74
NCBI Description (AL022373) putative protein [Arabidopsis thaliana]

Seq. No. 224477
Seq. ID LIB3166-011-P1-K1-F1
Method BLASTX
NCBI GI g498038
BLAST score 282
E value 2.0e-29
Match length 106
% identity 60
NCBI Description (L33792) lipid transfer protein [Senecio odorus]

Seq. No. 224478
Seq. ID LIB3166-011-P1-K1-F10
Method BLASTX
NCBI GI g3298441
BLAST score 270
E value 9.0e-24
Match length 103
% identity 58
NCBI Description (AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]

Seq. No. 224479
Seq. ID LIB3166-011-P1-K1-F12
Method BLASTX
NCBI GI g2982303
BLAST score 551
E value 9.0e-57
Match length 127
% identity 81
NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 224480
Seq. ID LIB3166-011-P1-K1-F3
Method BLASTX
NCBI GI g4490736
BLAST score 331
E value 6.0e-31
Match length 132
% identity 66
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 224481
Seq. ID LIB3166-011-P1-K1-F7
Method BLASTX
NCBI GI g629541
BLAST score 484
E value 8.0e-49
Match length 115
% identity 81
NCBI Description plasma membrane intrinsic protein 1c - Arabidopsis thaliana
>gi_472875_emb_CAA53476_(X75882) plasma membrane intrinsic
protein 1c [Arabidopsis thaliana]

Seq. No. 224482
Seq. ID LIB3166-011-P1-K1-F8
Method BLASTX
NCBI GI q3341679
BLAST score 274
E value 3.0e-24
Match length 82
% identity 70
NCBI Description (AC003672) dynamin-like protein phragmoplastin 12
[Arabidopsis thaliana]

Seq. No. 224483
Seq. ID LIB3166-011-P1-K1-F9
Method BLASTX
NCBI GI q3775997
BLAST score 391
E value 6.0e-38
Match length 90
% identity 84
NCBI Description (AJ010462) RNA helicase [Arabidopsis thaliana]

Seq. No. 224484
Seq. ID LIB3166-011-P1-K1-G1
Method BLASTX
NCBI GI g2511541
BLAST score 402
E value 1.0e-39
Match length 90
% identity 88
NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No. 224485
Seq. ID LIB3166-011-P1-K1-G12
Method BLASTX
NCBI GI g3901012
BLAST score 602
E value 1.0e-62
Match length 135
% identity 76
NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 224486
Seq. ID LIB3166-011-P1-K1-G2
Method BLASTX
NCBI GI g2961372
BLAST score 432
E value 8.0e-43
Match length 85
% identity 93
NCBI Description (AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_(AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 224487
Seq. ID LIB3166-011-P1-K1-G3
Method BLASTX

NCBI GI g4544403
BLAST score 624
E value 3.0e-65
Match length 139
% identity 81
NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase precursor [Arabidopsis thaliana]

Seq. No. 224488
Seq. ID LIB3166-011-P1-K1-G4
Method BLASTX
NCBI GI g1220196
BLAST score 508
E value 1.0e-51
Match length 112
% identity 85
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 224489
Seq. ID LIB3166-011-P1-K1-G9
Method BLASTX
NCBI GI g3941543
BLAST score 241
E value 2.0e-20
Match length 72
% identity 68
NCBI Description (AF069497) pelota [Arabidopsis thaliana]
>gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
[Arabidopsis thaliana]

Seq. No. 224490
Seq. ID LIB3166-011-P1-K1-H1
Method BLASTX
NCBI GI g3434967
BLAST score 204
E value 4.0e-16
Match length 85
% identity 53
NCBI Description (AB008103) ethylene responsive element binding factor 1
[Arabidopsis thaliana]

Seq. No. 224491
Seq. ID LIB3166-011-P1-K1-H4
Method BLASTX
NCBI GI g2982453
BLAST score 291
E value 3.0e-26
Match length 99
% identity 62
NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein
[Arabidopsis thaliana]

Seq. No. 224492
Seq. ID LIB3166-011-P1-K1-H9
Method BLASTX
NCBI GI g3885328
BLAST score 157

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E value 9.0e-11
Match length 83
% identity 40
NCBI Description (AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 224493
Seq. ID LIB3166-012-P1-K1-A4
Method BLASTX
NCBI GI g91035
BLAST score 608
E value 2.0e-63
Match length 127
% identity 93
NCBI Description laminin receptor homolog - mouse >gi_52853_emb_CAA29696_(X06406) protein p40 (AA 1 - 295) [Mus musculus]
>gi_228997_prf_1815216A laminin receptor [Cricetinae gen. sp.]

Seq. No. 224494
Seq. ID LIB3166-012-P1-K1-A5
Method BLASTX
NCBI GI g2894106
BLAST score 654
E value 8.0e-69
Match length 127
% identity 94
NCBI Description (Z78279) Collagen alpha1 [Rattus norvegicus]

Seq. No. 224495
Seq. ID LIB3166-012-P1-K1-A6
Method BLASTX
NCBI GI g3164123
BLAST score 643
E value 2.0e-67
Match length 126
% identity 94
NCBI Description (AJ224880) collagen alpha 2 type V [Rattus norvegicus]

Seq. No. 224496
Seq. ID LIB3166-012-P1-K1-A8
Method BLASTX
NCBI GI g127177
BLAST score 223
E value 2.0e-18
Match length 87
% identity 54
NCBI Description MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM (G2) (DTNB) (MLC-2) >gi_71706_pir_MORTL2 myosin L2 (DTNB) regulatory light chain precursor, skeletal muscle - rat
>gi_825539_emb_CAA25480_(X00975) MLC2 [Rattus norvegicus]

Seq. No. 224497
Seq. ID LIB3166-012-P1-K1-B10
Method BLASTX
NCBI GI g309233
BLAST score 413

E value 1.0e-40
Match length 79
% identity 100
NCBI Description (M24509) ferritin heavy chain [Mus musculus] >gi_1435203
(U58829) ferritin-H subunit [Rattus norvegicus]

Seq. No. 224498
Seq. ID LIB3166-012-P1-K1-B2
Method BLASTX
NCBI GI g1588365
BLAST score 382
E value 8.0e-37
Match length 104
% identity 74
NCBI Description signal peptidase:SUBUNIT=12kD [Homo sapiens]

Seq. No. 224499
Seq. ID LIB3166-012-P1-K1-B7
Method BLASTX
NCBI GI g2894106
BLAST score 337
E value 4.0e-32
Match length 66
% identity 98
NCBI Description (Z78279) Collagen alpha1 [Rattus norvegicus]

Seq. No. 224500
Seq. ID LIB3166-012-P1-K1-C1
Method BLASTX
NCBI GI g111946
BLAST score 407
E value 8.0e-40
Match length 84
% identity 88
NCBI Description matrix Gla protein precursor - rat

Seq. No. 224501
Seq. ID LIB3166-012-P1-K1-C10
Method BLASTX
NCBI GI g2135915
BLAST score 670
E value 1.0e-70
Match length 127
% identity 95
NCBI Description phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32)
precursor, mitochondrial - human >gi_1403050_emb_CAA63380
(X92720) phosphoenolpyruvate carboxykinase (GTP) [Homo sapiens]

Seq. No. 224502
Seq. ID LIB3166-012-P1-K1-C6
Method BLASTX
NCBI GI g4098993
BLAST score 474
E value 1.0e-47
Match length 121
% identity 79

NCBI Description (U81491) polyhomeotic 2 [Mus musculus]

Seq. No. 224503
Seq. ID LIB3166-012-P1-K1-C7
Method BLASTX
NCBI GI g417192
BLAST score 414
E value 1.0e-40
Match length 97
% identity 78
NCBI Description MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (MCP-3) (MONOCYTE CHEMOATTRACTANT PROTEIN 3) (INTERCRINE/CHEMOKINE MARC) (FIC PROTEIN) >gi_57938_emb_CAA78169_ (Z12297) intercrine [Mus musculus] >gi_547089_bbs_149941_ (S71251) monocyte chemotactic protein-3, MCP-3, Marc/Fic protein [mice, macrophage cell line WEHI-3, Peptide, 97 aa] [Mus sp.]

Seq. No. 224504
Seq. ID LIB3166-012-P1-K1-E11
Method BLASTX
NCBI GI g123651
BLAST score 506
E value 5.0e-62
Match length 134
% identity 96
NCBI Description HEAT SHOCK COGNATE 71 KD PROTEIN >gi_111759_pir_S07197 heat shock cognate protein hsc73 - rat
>gi_2119718_pir_JC4853 heat-shock protein 73 - mouse
>gi_56379_emb_CAA68265_ (Y00054) hsc73 [Rattus norvegicus]
>gi_204667_ (M11942) 70 kDa heat-shock-like protein [Rattus norvegicus] >gi_861213_ (U27129) heat shock 73 protein [Mus musculus]

Seq. No. 224505
Seq. ID LIB3166-012-P1-K1-E12
Method BLASTX
NCBI GI g3043917
BLAST score 345
E value 1.0e-32
Match length 113
% identity 63
NCBI Description (AF029844) elongation factor 1-beta homolog [Mus musculus]

Seq. No. 224506
Seq. ID LIB3166-012-P1-K1-E6
Method BLASTX
NCBI GI g114291
BLAST score 272
E value 1.0e-24
Match length 53
% identity 98
NCBI Description ARGININOSUCCINATE SYNTHASE (CITRULLINE--ASPARTATE LIGASE) >gi_68637_pir_AJRTRS argininosuccinate synthase (EC 6.3.4.5) - rat >gi_55767_emb_CAA30999_ (X12459) argininosuccinate synthetase (AA 1-412) [Rattus norvegicus] >gi_203016_ (M36708) argininosuccinate synthetase [Rattus norvegicus]

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Seq. No. 224507
Seq. ID LIB3166-012-P1-K1-F10
Method BLASTX
NCBI GI g137475
BLAST score 729
E value 1.0e-77
Match length 139
% identity 99
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
(32 KD ACCESSORY PROTEIN) (P39) >gi_89602_pir_A32123
H+-transporting ATPase (EC 3.6.1.35) polypeptide IV,
vacuolar - bovine

Seq. No. 224508
Seq. ID LIB3166-012-P1-K1-F11
Method BLASTX
NCBI GI g2833633
BLAST score 611
E value 1.0e-63
Match length 136
% identity 81
NCBI Description (AC003108) Unknown gene product [Homo sapiens]

Seq. No. 224509
Seq. ID LIB3166-012-P1-K1-F12
Method BLASTX
NCBI GI g543201
BLAST score 611
E value 1.0e-63
Match length 132
% identity 84
NCBI Description collagen alpha 1(I) chain precursor - mouse (fragments)

Seq. No. 224510
Seq. ID LIB3166-012-P1-K1-F3
Method BLASTX
NCBI GI g117505
BLAST score 193
E value 6.0e-15
Match length 71
% identity 56
NCBI Description CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
(CALBP) (CALCIUM-BINDING PROTEIN 3) (CABP3)
>gi_627974_pir_JH0819 calreticulin precursor - rat
>gi_55855_emb_CAA37446 (X53363) precursor (AA -17 to 399)
[Rattus norvegicus] >gi_488841_emb_CAA55890 (X79327)
calreticulin [Rattus norvegicus] >gi_1845572_dbj_BAA11345_
(D78308) calreticulin [Rattus norvegicus]

Seq. No. 224511
Seq. ID LIB3166-012-P1-K1-F4
Method BLASTX
NCBI GI g478811
BLAST score 232
E value 1.0e-19
Match length 74

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% identity 17
NCBI Description polyubiquitin - bovine >gi_645_emb_CAA79146_ (Z18245)
polyubiquitin [Bos taurus]

Seq. No. 224512
Seq. ID LIB3166-012-P1-K1-F9
Method BLASTX
NCBI GI g2961553
BLAST score 559
E value 9.0e-58
Match length 113
% identity 100
NCBI Description (AF049878) amyloid beta-peptide binding protein; ERAB
[Rattus norvegicus]

Seq. No. 224513
Seq. ID LIB3166-012-P1-K1-G10
Method BLASTX
NCBI GI g231671
BLAST score 156
E value 2.0e-10
Match length 31
% identity 94
NCBI Description PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR
>gi_284994_pir_A43291 collagen alpha 2(I) chain precursor
- mouse >gi_50489_emb_CAA41205_ (X58251) pro-alpha-2(I)
collagen [Mus musculus]

Seq. No. 224514
Seq. ID LIB3166-012-P1-K1-G8
Method BLASTX
NCBI GI g119146
BLAST score 628
E value 6.0e-68
Match length 135
% identity 96
NCBI Description ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
FACTOR TU) (EF-TU) >gi_90198_pir_JU0133 translation
elongation factor eEF-1 alpha chain - Chinese hamster
>gi_111601_pir_S21055 translation elongation factor eEF-1
alpha chain - rat >gi_56080_emb_CAA43378_ (X61043)
elongation factor 1 alpha [Rattus norvegicus]
>gi_56093_emb_CAA45122_ (X63561) elongation factor 1-alpha
[Rattus norvegicus] >gi_220279_dbj_BAA00409_ (D00522) EF-1
alpha [Cricetulus longicaudatus]

Seq. No. 224515
Seq. ID LIB3166-012-P1-K1-H12
Method BLASTX
NCBI GI g3123887
BLAST score 267
E value 1.0e-23
Match length 63
% identity 81
NCBI Description (AF027706) serine/threonine kinase RICK [Homo sapiens]
>gi_3264574 (AC004003) serine/threonine kinase RICK; match
to protein AF027706 (PID:g3123887) and mRNA AF027706

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(NID:g3123886) [Homo sapiens] >gi_3290172 (AF064824)
CARD-containing ICE associated kinase [Homo sapiens]
>gi_3342910 (AF078530) receptor interacting protein 2 [Homo
sapiens] >gi_4151948 (AF117829) serine/threonine kinase
RICK [Homo sapiens] >gi_4506537_ref_NP_003812.1_pRIP2_
UNKNOWN

Seq. No. 224516
Seq. ID LIB3166-012-P1-K1-H3
Method BLASTX
NCBI GI g809561
BLAST score 427
E value 3.0e-42
Match length 87
% identity 95
NCBI Description (X13055) gamma-actin [Mus musculus]

Seq. No. 224517
Seq. ID LIB3166-012-P1-K1-H6
Method BLASTX
NCBI GI g548747
BLAST score 312
E value 2.0e-32
Match length 71
% identity 92
NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi_1363320_pir_A53204
ribosomal protein L13a - rat >gi_460776_emb_CAA48343
(X68282) rat ribosomal protein L13a [Rattus norvegicus]

Seq. No. 224518
Seq. ID LIB3166-012-P1-K1-H7
Method BLASTX
NCBI GI g1213490
BLAST score 200
E value 3.0e-20
Match length 56
% identity 95
NCBI Description (U42719) C4 complement protein [Rattus norvegicus]

Seq. No. 224519
Seq. ID LIB3166-012-P1-K1-H8
Method BLASTX
NCBI GI g1173177
BLAST score 471
E value 1.0e-47
Match length 93
% identity 96
NCBI Description 40S RIBOSOMAL PROTEIN S10 >gi_1362933_pir_S55918 ribosomal
protein S10 - human >gi_550025 (U14972) ribosomal protein
S10 [Homo sapiens] >gi_1096944_prf_2113200G ribosomal
protein S10 [Homo sapiens]
>gi_4506679_ref_NP_001005.1_pRPS10_ ribosomal protein S10

Seq. No. 224520
Seq. ID LIB3166-013-P1-K1-A12
Method BLASTX
NCBI GI g2443757

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BLAST score 306
E value 3.0e-28
Match length 90
% identity 67
NCBI Description (AF020434) cyclophilin [Arabidopsis thaliana]

Seq. No. 224521
Seq. ID LIB3166-013-P1-K1-A4
Method BLASTX
NCBI GI g4510376
BLAST score 362
E value 2.0e-34
Match length 144
% identity 54
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 224522
Seq. ID LIB3166-013-P1-K1-B12
Method BLASTX
NCBI GI g4107276
BLAST score 261
E value 1.0e-22
Match length 59
% identity 90
NCBI Description (X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No. 224523
Seq. ID LIB3166-013-P1-K1-B2
Method BLASTX
NCBI GI g3451072
BLAST score 240
E value 2.0e-20
Match length 72
% identity 58
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 224524
Seq. ID LIB3166-013-P1-K1-B6
Method BLASTX
NCBI GI g113363
BLAST score 511
E value 2.0e-54
Match length 129
% identity 77
NCBI Description ALCOHOL DEHYDROGENASE 1 >gi_279445_pir_DEPJA1 alcohol dehydrogenase (EC 1.1.1.1) 1 - garden petunia >gi_20506_emb_CAA38039_ (X54106) alcohol dehydrogenase [Petunia x hybrida]

Seq. No. 224525
Seq. ID LIB3166-013-P1-K1-B7
Method BLASTX
NCBI GI g4314355
BLAST score 305
E value 8.0e-28
Match length 88
% identity 60

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NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	224526
Seq. ID	LIB3166-013-P1-K1-B9
Method	BLASTX
NCBI GI	g2522534
BLAST score	185
E value	2.0e-14
Match length	86
% identity	48
NCBI Description	(AF027302) TNF-alpha

Seq. No.	224527
Seq. ID	LIB3166-013-P1-K1-C1
Method	BLASTX
NCBI GI	g3269293
BLAST score	276
E value	1.0e-24
Match length	103
% identity	57
NCBI Description	(AL030978) putative

Seq. No.	224528
Seq. ID	LIB3166-013-P1-K1-C11
Method	BLASTX
NCBI GI	g2961378
BLAST score	574
E value	2.0e-59
Match length	143
% identity	39
NCBI Description	(AL022141) putative p

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Seq. No.          224529
Seq. ID          LIB3166-013-P1-K1-C5
Method          BLASTX
NCBI GI          g3021489
BLAST score      164
E value          2.0e-15
Match length     88
% identity        62
NCBI Description (AJ224934) histone H

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Seq. No. 224530
Seq. ID LIB3166-013-P1-K1-C6
Method BLASTX
NCBI GI g3122388
BLAST score 610
E value 1.0e-63
Match length 131
% identity 31
NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 224531
Seq. ID LIB3166-013-P1-K1-C7
Method BLASTX
NCBI GI q4510345

BLAST score 275
E value 2.0e-24
Match length 63
% identity 75
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 224532
Seq. ID LIB3166-013-P1-K1-C9
Method BLASTX
NCBI GI g3660552
BLAST score 221
E value 5.0e-18
Match length 51
% identity 76
NCBI Description (AB013817) DREB1C [Arabidopsis thaliana]
>gi_3738228_dbj_BAA33793_ (AB007789) DREB1C [Arabidopsis thaliana] >gi_3907541_ (AF062925) transcriptional activator CBF1 homolog [Arabidopsis thaliana]
>gi_4322228_gb_AAD15976_ (AF074601) CRT/DRE binding factor 2 [Arabidopsis thaliana]

Seq. No. 224533
Seq. ID LIB3166-013-P1-K1-D2
Method BLASTX
NCBI GI g3367593
BLAST score 251
E value 2.0e-21
Match length 120
% identity 58
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
>gi_3805841_emb_CAA21461_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 224534
Seq. ID LIB3166-013-P1-K1-D3
Method BLASTX
NCBI GI g1168734
BLAST score 503
E value 4.0e-51
Match length 133
% identity 77
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD)
>gi_288753_emb_CAA79622_ (Z19568) cinnamyl alcohol dehydrogenase [Populus deltoides]

Seq. No. 224535
Seq. ID LIB3166-013-P1-K1-E10
Method BLASTX
NCBI GI g3894173
BLAST score 146
E value 3.0e-09
Match length 32
% identity 75
NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224536
Seq. ID LIB3166-013-P1-K1-E11

Method BLASTX
NCBI GI g3123271
BLAST score 262
E value 3.0e-23
Match length 59
% identity 86
NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052)
ribosomal protein S6 [Arabidopsis thaliana]

Seq. No. 224537
Seq. ID LIB3166-013-P1-K1-E5
Method BLASTX
NCBI GI g3193292
BLAST score 517
E value 9.0e-53
Match length 122
% identity 85
NCBI Description (AF069298) similar to ATPases associated with various
cellular activites (Pfam: AAA.hmm, score: 230.91)
[Arabidopsis thaliana]

Seq. No. 224538
Seq. ID LIB3166-013-P1-K1-E9
Method BLASTX
NCBI GI g2754746
BLAST score 309
E value 2.0e-28
Match length 143
% identity 50
NCBI Description (U85448) sucrose-phosphate synthase [Actinidia deliciosa]

Seq. No. 224539
Seq. ID LIB3166-013-P1-K1-F1
Method BLASTX
NCBI GI g2736288
BLAST score 146
E value 3.0e-09
Match length 33
% identity 79
NCBI Description (AF031080) isopentenyl diphosphate isomerase II
[Camptotheca acuminata]

Seq. No. 224540
Seq. ID LIB3166-013-P1-K1-F10
Method BLASTX
NCBI GI g1332579
BLAST score 267
E value 5.0e-24
Match length 72
% identity 7
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 224541
Seq. ID LIB3166-013-P1-K1-F12
Method BLASTX
NCBI GI g1350777
BLAST score 324

E value 4.0e-30
Match length 75
% identity 87
NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012)
ribosomal protein L9 [Oryza sativa]

Seq. No. 224542
Seq. ID LIB3166-013-P1-K1-F2
Method BLASTX
NCBI GI g4090533
BLAST score 460
E value 3.0e-46
Match length 101
% identity 82
NCBI Description (U68215) ACC oxidase [Carica papaya]

Seq. No. 224543
Seq. ID LIB3166-013-P1-K1-F6
Method BLASTX
NCBI GI g2146739
BLAST score 262
E value 8.0e-23
Match length 118
% identity 51
NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
(U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No. 224544
Seq. ID LIB3166-013-P1-K1-F7
Method BLASTX
NCBI GI g400976
BLAST score 426
E value 1.0e-48
Match length 108
% identity 96
NCBI Description RAS-RELATED PROTEIN RHA1 >gi_478671_pir_S23727 GTP-binding
protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_
(X59152) RHA1 [Arabidopsis thaliana]
>gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein
[Arabidopsis thaliana]

Seq. No. 224545
Seq. ID LIB3166-013-P1-K1-F9
Method BLASTX
NCBI GI g1888357
BLAST score 499
E value 1.0e-50
Match length 123
% identity 76
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
>gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
precursor [Arabidopsis thaliana]

Seq. No. 224546
Seq. ID LIB3166-013-P1-K1-G10
Method BLASTX
NCBI GI g2673910

BLAST score 148
E value 2.0e-09
Match length 67
% identity 54
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224547
Seq. ID LIB3166-013-P1-K1-G12
Method BLASTX
NCBI GI g1061420
BLAST score 512
E value 4.0e-52
Match length 127
% identity 82
NCBI Description (U38965) p-type H+-ATPase [Vicia faba]

Seq. No. 224548
Seq. ID LIB3166-013-P1-K1-G2
Method BLASTX
NCBI GI g3341468
BLAST score 170
E value 5.0e-12
Match length 85
% identity 45
NCBI Description (AJ009594) Dof zinc finger protein [Nicotiana tabacum]

Seq. No. 224549
Seq. ID LIB3166-013-P1-K1-G3
Method BLASTX
NCBI GI g1655653
BLAST score 113
E value 6.0e-09
Match length 100
% identity 38
NCBI Description (Z81368) hypothetical protein Rv2406c [Mycobacterium tuberculosis]

Seq. No. 224550
Seq. ID LIB3166-013-P1-K1-G5
Method BLASTX
NCBI GI g3136336
BLAST score 415
E value 6.0e-41
Match length 81
% identity 52
NCBI Description (AF064552) calmodulin; Cam [Apium graveolens]

Seq. No. 224551
Seq. ID LIB3166-013-P1-K1-G6
Method BLASTX
NCBI GI g2281090
BLAST score 394
E value 3.0e-38
Match length 115
% identity 65
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

090606-101000

Seq. No. 224552
Seq. ID LIB3166-013-P1-K1-G7
Method BLASTX
NCBI GI g629722
BLAST score 175
E value 1.0e-12
Match length 122
% identity 35
NCBI Description finger protein pcp1 - potato >gi_563623_emb_CAA57772_(X82328) putative DNA/RNA binding protein [Solanum tuberosum]

Seq. No. 224553
Seq. ID LIB3166-013-P1-K1-G8
Method BLASTX
NCBI GI g4406787
BLAST score 388
E value 1.0e-37
Match length 102
% identity 77
NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No. 224554
Seq. ID LIB3166-013-P1-K1-G9
Method BLASTX
NCBI GI g3892059
BLAST score 270
E value 1.0e-23
Match length 143
% identity 48
NCBI Description (AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 224555
Seq. ID LIB3166-013-P1-K1-H10
Method BLASTX
NCBI GI g2983778
BLAST score 164
E value 2.0e-11
Match length 116
% identity 36
NCBI Description (AE000736) hypothetical protein [Aquifex aeolicus]

Seq. No. 224556
Seq. ID LIB3166-013-P1-K1-H5
Method BLASTX
NCBI GI g4512694
BLAST score 238
E value 6.0e-20
Match length 133
% identity 41
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224557
Seq. ID LIB3166-013-P1-K1-H7
Method BLASTX
NCBI GI g464621

BLAST score 278
E value 9.0e-25
Match length 104
% identity 54
NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir_S28586
ribosomal protein ML16 - common ice plant
>gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
[Mesembryanthemum crystallinum]

Seq. No. 224558
Seq. ID LIB3166-013-P1-K1-H9
Method BLASTX
NCBI GI g3334320
BLAST score 482
E value 1.0e-48
Match length 108
% identity 92
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553)
ribosome-associated protein p40 [Glycine max]

Seq. No. 224559
Seq. ID LIB3166-014-P1-K1-A1
Method BLASTX
NCBI GI g3540195
BLAST score 441
E value 8.0e-44
Match length 135
% identity 31
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 224560
Seq. ID LIB3166-014-P1-K1-A10
Method BLASTX
NCBI GI g4467147
BLAST score 194
E value 5.0e-22
Match length 110
% identity 56
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 224561
Seq. ID LIB3166-014-P1-K1-A12
Method BLASTX
NCBI GI g541546
BLAST score 306
E value 6.0e-38
Match length 110
% identity 16
NCBI Description ubiquitin precursor - Volvox carteri
>gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox
carteri]

Seq. No. 224562
Seq. ID LIB3166-014-P1-K1-A4
Method BLASTX
NCBI GI g2982303
BLAST score 574

E value 2.0e-59
 Match length 131
 % identity 79
 NCBI Description (AF051236) hypothetical protein [Picea mariana]

 Seq. No. 224563
 Seq. ID LIB3166-014-P1-K1-A8
 Method BLASTX
 NCBI GI g3264767
 BLAST score 500
 E value 9.0e-51
 Match length 119
 % identity 76
 NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

 Seq. No. 224564
 Seq. ID LIB3166-014-P1-K1-B1
 Method BLASTX
 NCBI GI g4454050
 BLAST score 301
 E value 2.0e-27
 Match length 79
 % identity 66
 NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

 Seq. No. 224565
 Seq. ID LIB3166-014-P1-K1-B10
 Method BLASTX
 NCBI GI g2190419
 BLAST score 202
 E value 8.0e-16
 Match length 109
 % identity 40
 NCBI Description (Y13632) dem [Lycopersicon esculentum]

 Seq. No. 224566
 Seq. ID LIB3166-014-P1-K1-B2
 Method BLASTX
 NCBI GI g1432056
 BLAST score 184
 E value 1.0e-13
 Match length 110
 % identity 45
 NCBI Description (U56834) WRKY3 [Petroselinum crispum]

 Seq. No. 224567
 Seq. ID LIB3166-014-P1-K1-B5
 Method BLASTX
 NCBI GI g2318137
 BLAST score 590
 E value 2.0e-61
 Match length 117
 % identity 97
 NCBI Description (AF014052) Mg protoporphyrin IX chelatase [Nicotiana tabacum]

 Seq. No. 224568

Seq. ID LIB3166-014-P1-K1-B6
Method BLASTX
NCBI GI g2970654
BLAST score 184
E value 8.0e-14
Match length 83
% identity 58
NCBI Description (AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No. 224569
Seq. ID LIB3166-014-P1-K1-B7
Method BLASTX
NCBI GI g2970654
BLAST score 215
E value 2.0e-17
Match length 97
% identity 57
NCBI Description (AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No. 224570
Seq. ID LIB3166-014-P1-K1-B9
Method BLASTX
NCBI GI g1814424
BLAST score 575
E value 2.0e-59
Match length 134
% identity 78
NCBI Description (U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No. 224571
Seq. ID LIB3166-014-P1-K1-C12
Method BLASTX
NCBI GI g231675
BLAST score 163
E value 1.0e-23
Match length 64
% identity 86
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_282955_pir_S23525
cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - common
tobacco >gi_19839_emb_CAA44216 (X62343) cinnamyl-alcohol
dehydrogenase [Nicotiana tabacum]

Seq. No. 224572
Seq. ID LIB3166-014-P1-K1-C2
Method BLASTX
NCBI GI g4204293
BLAST score 503
E value 4.0e-51
Match length 125
% identity 76
NCBI Description (AC003027) lcl_prt_seq No definition line found
[Arabidopsis thaliana]

Seq. No. 224573
Seq. ID LIB3166-014-P1-K1-C6

Method BLASTX
NCBI GI g2980770
BLAST score 410
E value 3.0e-40
Match length 125
% identity 66
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 224574
Seq. ID LIB3166-014-P1-K1-C7
Method BLASTX
NCBI GI g2980770
BLAST score 420
E value 2.0e-41
Match length 133
% identity 65
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 224575
Seq. ID LIB3166-014-P1-K1-C8
Method BLASTX
NCBI GI g4512651
BLAST score 520
E value 4.0e-53
Match length 133
% identity 68
NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 224576
Seq. ID LIB3166-014-P1-K1-C9
Method BLASTX
NCBI GI g289920
BLAST score 384
E value 3.0e-37
Match length 102
% identity 75
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum]

Seq. No. 224577
Seq. ID LIB3166-014-P1-K1-D11
Method BLASTX
NCBI GI g1652104
BLAST score 330
E value 8.0e-31
Match length 125
% identity 51
NCBI Description (D90902) hypothetical protein [Synechocystis sp.]

Seq. No. 224578
Seq. ID LIB3166-014-P1-K1-D12
Method BLASTX
NCBI GI g2129921
BLAST score 179
E value 3.0e-13
Match length 48

% identity 73
NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694
(U12573) putative [Catharanthus roseus]

Seq. No. 224579
Seq. ID LIB3166-014-P1-K1-D3
Method BLASTX
NCBI GI g2262111
BLAST score 197
E value 3.0e-15
Match length 75
% identity 55
NCBI Description (AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]

Seq. No. 224580
Seq. ID LIB3166-014-P1-K1-D4
Method BLASTX
NCBI GI g1769887
BLAST score 556
E value 3.0e-57
Match length 129
% identity 85
NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No. 224581
Seq. ID LIB3166-014-P1-K1-D9
Method BLASTX
NCBI GI g1906828
BLAST score 432
E value 8.0e-43
Match length 104
% identity 84
NCBI Description (Y11828) heat shock protein [Arabidopsis thaliana]

Seq. No. 224582
Seq. ID LIB3166-014-P1-K1-E1
Method BLASTX
NCBI GI g1370180
BLAST score 233
E value 2.0e-19
Match length 54
% identity 87
NCBI Description (Z73939) RAB5B [Lotus japonicus]

Seq. No. 224583
Seq. ID LIB3166-014-P1-K1-E10
Method BLASTX
NCBI GI g4008441
BLAST score 379
E value 1.0e-36
Match length 102
% identity 69
NCBI Description (AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 224584
Seq. ID LIB3166-014-P1-K1-E11
Method BLASTX
NCBI GI g3915847
BLAST score 371
E value 1.0e-35
Match length 81
% identity 86
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 224585
Seq. ID LIB3166-014-P1-K1-E3
Method BLASTX
NCBI GI g3024017
BLAST score 430
E value 2.0e-42
Match length 83
% identity 98
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No. 224586
Seq. ID LIB3166-014-P1-K1-E4
Method BLASTX
NCBI GI g2662415
BLAST score 284
E value 2.0e-25
Match length 76
% identity 61
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No. 224587
Seq. ID LIB3166-014-P1-K1-E5
Method BLASTX
NCBI GI g3063396
BLAST score 286
E value 1.0e-42
Match length 110
% identity 82
NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 224588
Seq. ID LIB3166-014-P1-K1-E8
Method BLASTX
NCBI GI g2244835
BLAST score 298
E value 4.0e-27
Match length 91
% identity 66
NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 224589
Seq. ID LIB3166-014-P1-K1-E9
Method BLASTX

NCBI GI g3738325
BLAST score 403
E value 2.0e-39
Match length 110
% identity 71
NCBI Description (AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No. 224590
Seq. ID LIB3166-014-P1-K1-F1
Method BLASTX
NCBI GI g2924777
BLAST score 376
E value 3.0e-36
Match length 130
% identity 6
NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 224591
Seq. ID LIB3166-014-P1-K1-F10
Method BLASTX
NCBI GI g2662415
BLAST score 173
E value 2.0e-12
Match length 56
% identity 54
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No. 224592
Seq. ID LIB3166-014-P1-K1-F2
Method BLASTX
NCBI GI g1351271
BLAST score 331
E value 6.0e-31
Match length 118
% identity 62
NCBI Description TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
>gi_1084309_pir_S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No. 224593
Seq. ID LIB3166-014-P1-K1-F3
Method BLASTX
NCBI GI g1814424
BLAST score 582
E value 2.0e-60
Match length 134
% identity 79
NCBI Description (U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No. 224594
Seq. ID LIB3166-014-P1-K1-F8
Method BLASTX
NCBI GI g115484

BLAST score	555
E value	3.0e-57
Match length	108
% identity	59
NCBI Description	CALMODULIN 1 >gi_71684_pir_MCPZDC calmodulin - carrot >gi_478632_pir_S22971 calmodulin - trumpet lily >gi_541839_pir_S40301 calmodulin - Red bryony >gi_2129970_pir_S70768 calmodulin CAM81 - garden petunia >gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota] >gi_19447_emb_CAA78301_ (Z12839) calmodulin [Lilium longiflorum] >gi_169207_ (M80836) calmodulin [Petunia hybrida] >gi_308900_ (L18912) calmodulin [Lilium longiflorum] >gi_505154_emb_CAA43143_ (X60738) Calmodulin [Malus domestica] >gi_535444_ (U13882) calmodulin [Pisum sativum] >gi_445602_prf_1909349A calmodulin [Daucus carota]
Seq. No.	224595
Seq. ID	LIB3166-014-P1-K1-F9
Method	BLASTX
NCBI GI	g1709930
BLAST score	359
E value	2.0e-35
Match length	94
% identity	81
NCBI Description	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE PRECURSOR (AIR CARBOXYLASE) (AIRC) >gi_629656_pir_S43322 phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) - moth bean >gi_349159_ (L22584) 5-aminoimidazole ribonucleotide carboxylase [Vigna aconitifolia]
Seq. No.	224596
Seq. ID	LIB3166-014-P1-K1-G1
Method	BLASTX
NCBI GI	g2809251
BLAST score	152
E value	2.0e-10
Match length	34
% identity	74
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]
Seq. No.	224597
Seq. ID	LIB3166-014-P1-K1-G10
Method	BLASTX
NCBI GI	g2245087
BLAST score	218
E value	1.0e-17
Match length	86
% identity	44
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224598
Seq. ID	LIB3166-014-P1-K1-G5
Method	BLASTX
NCBI GI	g4127456
BLAST score	303
E value	1.0e-27

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Match length 114
 % identity 59
 NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

 Seq. No. 224599
 Seq. ID LIB3166-014-P1-K1-G6
 Method BLASTX
 NCBI GI g2088651
 BLAST score 482
 E value 1.0e-48
 Match length 123
 % identity 70
 NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

 Seq. No. 224600
 Seq. ID LIB3166-014-P1-K1-G7
 Method BLASTX
 NCBI GI g2088651
 BLAST score 432
 E value 8.0e-43
 Match length 118
 % identity 66
 NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

 Seq. No. 224601
 Seq. ID LIB3166-014-P1-K1-G9
 Method BLASTX
 NCBI GI g3212859
 BLAST score 505
 E value 2.0e-51
 Match length 112
 % identity 55
 NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]

 Seq. No. 224602
 Seq. ID LIB3166-014-P1-K1-H1
 Method BLASTX
 NCBI GI g2191136
 BLAST score 312
 E value 1.0e-28
 Match length 110
 % identity 60
 NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

 Seq. No. 224603
 Seq. ID LIB3166-014-P1-K1-H10
 Method BLASTX
 NCBI GI g4510381
 BLAST score 219
 E value 7.0e-18
 Match length 105
 % identity 52

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 224604
Seq. ID LIB3166-014-P1-K1-H11
Method BLASTX
NCBI GI g2760322
BLAST score 356
E value 7.0e-34
Match length 113
% identity 56

NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No. 224605
Seq. ID LIB3166-014-P1-K1-H2
Method BLASTX
NCBI GI g4049349
BLAST score 363
E value 1.0e-34
Match length 102
% identity 71

NCBI Description (AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No. 224606
Seq. ID LIB3166-014-P1-K1-H6
Method BLASTX
NCBI GI g2209332
BLAST score 365
E value 7.0e-35
Match length 102
% identity 73

NCBI Description (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] >gi_3927828 (AC005727) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana]

Seq. No. 224607
Seq. ID LIB3166-014-P1-K1-H8
Method BLASTX
NCBI GI g1237250
BLAST score 545
E value 5.0e-56
Match length 133
% identity 77

NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No. 224608
Seq. ID LIB3166-014-P1-K1-H9
Method BLASTX
NCBI GI g3269292
BLAST score 231
E value 3.0e-19
Match length 64
% identity 66

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 224609
Seq. ID LIB3166-015-P1-K1-A2

Method	BLASTX
NCBI GI	g3885334
BLAST score	502
E value	7.0e-51
Match length	147
% identity	71
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]
Seq. No.	224610
Seq. ID	LIB3166-015-P1-K1-A4
Method	BLASTX
NCBI GI	g417103
BLAST score	498
E value	1.0e-50
Match length	111
% identity	94
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]
Seq. No.	224611
Seq. ID	LIB3166-015-P1-K1-A7
Method	BLASTX
NCBI GI	g4559388
BLAST score	420
E value	3.0e-41
Match length	132
% identity	51
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224612
Seq. ID	LIB3166-015-P1-K1-B1
Method	BLASTX
NCBI GI	g3759184
BLAST score	351
E value	3.0e-33
Match length	104
% identity	66
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

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Seq. No.	224613
Seq. ID	LIB3166-015-P1-K1-B2
Method	BLASTX
NCBI GI	g132944
BLAST score	215
E value	5.0e-22
Match length	92
% identity	63
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir_JQ0772 ribosomal protein L3 (ARP2) - <i>Arabidopsis thaliana</i> >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.	224614
Seq. ID	LIB3166-015-P1-K1-B4
Method	BLASTX
NCBI GI	g3420049
BLAST score	172
E value	3.0e-12
Match length	131
% identity	40
NCBI Description	(AC004680) putative protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	224615
Seq. ID	LIB3166-015-P1-K1-B5
Method	BLASTX
NCBI GI	g2191136
BLAST score	312
E value	1.0e-28
Match length	110
% identity	60
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by <i>A. thaliana</i> cDNA T46230; coded for by <i>A. thaliana</i> cDNA H76538; coded for by <i>A. thaliana</i> cDNA H76290 [Arabidopsis thaliana]
Seq. No.	224616
Seq. ID	LIB3166-015-P1-K1-C10
Method	BLASTX
NCBI GI	g3953463
BLAST score	210
E value	1.0e-16
Match length	60
% identity	60
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]
Seq. No.	224617
Seq. ID	LIB3166-015-P1-K1-C12
Method	BLASTX
NCBI GI	g728906
BLAST score	330
E value	8.0e-31
Match length	126
% identity	55
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 5 >gi_1077722_pir_S50669 hypothetical protein YER166w - yeast (<i>Saccharomyces cerevisiae</i>) >gi_603407 (U18922)